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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-712-819d-13

Perfect score: 31

Sequence: 1 LTKLRSR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	18	58.1	5	3	US-08-981-122-65
2	18	58.1	7	3	US-09-173-941-72
3	18	58.1	7	4	US-09-423-468A-6
4	18	58.1	7	4	US-09-494-190-72
5	17	54.8	6	2	US-08-637-759B-219
6	17	54.8	6	3	US-08-871-355A-219
7	17	54.8	6	3	US-09-201-945-219
8	17	54.8	7	2	US-08-968-676-70
9	16	51.6	6	4	US-09-428-082B-532
10	16	51.6	7	1	US-08-239-854-1
11	16	51.6	7	1	US-08-239-854-2
12	16	51.6	7	1	US-08-346-333-24
13	16	51.6	7	2	US-08-968-676-117
14	16	51.6	7	2	US-08-968-676-121
15	16	51.6	7	5	PCT-US91-07506-24
16	15	48.4	6	1	US-08-066-325-144
17	15	48.4	6	2	US-08-177-109A-42
18	15	48.4	6	2	US-08-687-706-42
19	15	48.4	6	2	US-08-482-228-180
20	15	48.4	6	3	US-08-482-528-180
21	15	48.4	6	4	US-09-383-062-35
22	15	48.4	6	5	PCT-US95-08354A-9
23	15	48.4	6	6	5342922-6
24	15	48.4	7	2	US-08-968-676-4
25	15	48.4	7	2	US-08-968-676-23
26	15	48.4	7	2	US-08-545-745-4
27	15	48.4	7	3	US-08-654-623-69

28	15	48.4	7	3	US-09-173-941-62	Sequence 62, Appl
29	15	48.4	7	3	US-09-173-941-66	Sequence 66, Appl
30	15	48.4	7	3	US-09-173-941-67	Sequence 67, Appl
31	15	48.4	7	3	US-09-173-941-68	Sequence 68, Appl
32	15	48.4	7	3	US-09-139-802-76	Sequence 76, Appl
33	15	48.4	7	3	US-09-268-992-78	Sequence 78, Appl
34	15	48.4	7	3	US-09-657-474-78	Sequence 4, Appl
35	15	48.4	7	4	US-09-396-813-4	Sequence 76, Appl
36	15	48.4	7	4	US-09-659-786-76	Sequence 66, Appl
37	15	48.4	7	4	US-08-926-914-76	Sequence 62, Appl
38	15	48.4	7	4	US-09-494-190-62	Sequence 66, Appl
39	15	48.4	7	4	US-09-494-190-66	Sequence 67, Appl
40	15	48.4	7	4	US-09-494-190-67	Sequence 68, Appl
41	15	48.4	7	4	US-09-771-415-12	Sequence 12, Appl
42	15	48.4	7	4	US-08-305-871A-17	Sequence 17, Appl
43	14	45.2	4	1	US-08-788-822A-1	Sequence 1, Appl
44	14	45.2	4	4	US-08-409-199-7	Sequence 7, Appl
45	14	45.2	5	1		

ALIGNMENTS

RESULT 1

US-08-981-122-65

; Sequence 65, Application US/08981122B

; Patent No. 6127339

; GENERAL INFORMATION:

; APPLICANT: Hatanaka, Yoshihiro

; TITLE OF INVENTION: Peptide for binding thereto a low density lipoprotein

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/08/981.122B

; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: JP 7-176904

; PRIOR FILING DATE: 1995-06-21

; PRIOR APPLICATION NUMBER: PCT/JP96/01734

; PRIOR FILING DATE: 1996-06-21

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 65

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence of a peptide synthesized in Comparative Example 1 from Patent No. 6127339

; OTHER INFORMATION: L-form P-noc amino acids by solid phase method using a

; OTHER INFORMATION: multipetide synthesizing system (RAMPS)

US-08-981-122-65

Query Match 58.1%; Score 18; DB 3; Length 5;

Best Local Similarity 60.0%; Pred. No. 3.8e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKL 5

Db 1 LTKM 5

RESULT 2

US-09-173-941-72

; Sequence 72, Application US/09173941

; Patent No. 6140081

; GENERAL INFORMATION:

; APPLICANT: BARBAS, Carlos P.

; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN

; FILE REFERENCE: NOV0081S

; CURRENT APPLICATION NUMBER: US/09/173,941

; CURRENT FILING DATE: 1998-10-16

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 72

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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: codon binding sequence
US-09-173-941-72

Query Match          58.1%; Score 18; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7
Db 4 KLSR 7

RESULT 3
US-09-423-468A-6
; Sequence 6, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Brassica oleracea
US-09-423-468A-6

Query Match          58.1%; Score 18; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TIELSK 7

RESULT 4
US-09-494-190-72
; Sequence 72, Application US/09494190
; Patent No. 6610512
; GENERAL INFORMATION:
; APPLICANT: BARBAS, Carlos F.
; TITLE OF INVENTION: ZINC FINGER BINDING DOMAINS FOR GNN
; FILE REFERENCE: TSRI 645.2
; CURRENT APPLICATION NUMBER: US/09/494,190
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: EP/99/07742
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/173,941
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:phase display
; OTHER INFORMATION: selected and mutagenized

US-09-494-190-72

Query Match          54.8%; Score 17; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLSR 7
Db 2 LKLMR 6

RESULT 6
US-08-871-355A-219
; Sequence 219, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
```

NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871.355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMs 101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-219

Query Match 54.8%; Score 17; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLSR 7
Db 2 LKLMR 6

RESULT 7
US-09-201-945-219
Sequence 219, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMs 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-219

Query Match 54.8%; Score 17; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLSR 7
Db 2 LKLMR 6

RESULT 8
US-08-968-676-70
Sequence 70, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-968-676-70

Query Match 54.8%; Score 17; DB 2; Length 7;

Thu Nov 4 07:26:53 2004

us-09-712-819d-13.closed.ra1

```
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 1 LRLKLPK 7

RESULT 9
US-09-428-082B-532
; Sequence 532, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 532
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ANTIPATHOGENIC PEPTIDE
US-09-428-082B-532

Query Match 51.6%; Score 16; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKL 5
Db 2 LILKL 6

RESULT 10
US-08-239-854-1
; Sequence 1, Application US/08239854
; Patent No. 5624900
; GENERAL INFORMATION:
; APPLICANT: Suda, Tatsuo
; APPLICANT: Abe, Etsuko
; APPLICANT: Tanihara, Masao
; APPLICANT: Fujiwara, Chie
; TITLE OF INVENTION: Peptide or Its Salts
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,854
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/752,426
; FILING DATE:
; APPLICATION NUMBER: JP 233,571/90
; FILING DATE: 03-SRP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 320,000/90
; FILING DATE: 24-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324,956/90
; FILING DATE: 26-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5624900man F.
; REGISTRATION NUMBER: 24,618

Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTLKLS 6
Db 2 LRLKIS 7

RESULT 11
US-08-239-854-2
; Sequence 2, Application US/08239854
; Patent No. 5624900
; GENERAL INFORMATION:
; APPLICANT: Suda, Tatsuo
; APPLICANT: Abe, Etsuko
; APPLICANT: Tanihara, Masao
; APPLICANT: Fujiwara, Chie
; TITLE OF INVENTION: Peptide or Its Salts
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,854
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/752,426
; FILING DATE:
; APPLICATION NUMBER: JP 233,571/90
; FILING DATE: 03-SRP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 320,000/90
; FILING DATE: 24-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324,956/90
; FILING DATE: 26-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5624900man F.
; REGISTRATION NUMBER: 24,618

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLKLS 6
Db 2 LRLKIS 7
```


REFERENCE/DOCKET NUMBER: 363-279-0
TELEPHONE: (703) 521-4500
TELEFAX: (703) 486-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-239-854-2

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKLS 6
DB 2 LQIKS 7

RESULT 12
US-08-346-333-24
Sequence 24, Application US/08346333
Patent No. 5677153
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Palzkill, Timothy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on interaction of
TITLE OF INVENTION: encoded modified polypeptides with target substrates.
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,333
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/039,501
FILING DATE:
APPLICATION NUMBER: US 07/602,158
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-53469/RFT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-333-24

Query Match 51.6%; Score 16; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKL 5
DB 2 TLKI 5

RESULT 13
US-08-968-676-117
Sequence 117, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
OTHER INFORMATION: /note= "The Xaa at position 2 is the D-
US-08-968-676-117

Query Match 51.6%; Score 16; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LTKLSR 7
DB 1 LXXKLPK 7

RESULT 14
US-08-968-676-121
Sequence 121, Application US/08968676
Patent No. 5919639
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.

STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: RHH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
OTHER INFORMATION: /note="The Xaa at position 6 is the D-
OTHER INFORMATION: amino acid of Pro."
US-08-968-676-121

Query Match 51.6%; Score 16; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LTKLSR 7
Db 1 LRMKLKK 7

RESULT 15
PCT-US91-07506-24
Sequence 24, Application PC/TUS9107506
GENERAL INFORMATION:
APPLICANT: Botstein, David
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on interaction of
TITLE OF INVENTION: encoded modified polypeptides with target substrates.
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07506
FILING DATE: 19911021
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP-53469-PC/RFT

Query Match 51.6%; Score 16; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LTKLSR 7
Db 1 LRMKLKK 7

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US91-07506-24
Query Match 51.6%; Score 16; DB 5; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLKL 5
Db 2 TLKI 5
Search completed: November 4, 2004, 01:25:37
Job time : 25.6667 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	41.9	7	S19630	ribosomal protein
2	11	35.5	3	T13892	cytochrome-c oxida
3	11	35.5	4	T46627	hypothetical prote
4	11	35.5	5	E42364	flagellar protein
5	11	35.5	6	I49424	cytotoxic T-lympho
6	11	35.5	7	JN0859	peptidyl-dipectida
7	11	35.5	7	A28709	phosphonoacetaldeh
8	11	35.5	7	E48394	glycoprotein compo
9	11	35.5	7	I48086	DNA topoisomerase
10	11	35.5	7	E48394	major fat-globule
11	10	32.3	4	I45005	hypothetical prote
12	10	32.3	5	T14910	hypothetical prote
13	10	32.3	6	I48126	alpha-tubulin - Ch
14	10	32.3	6	B33932	Ig mu chain D regi
15	10	32.3	7	PN0649	pullulanase (EC 3.
16	10	32.3	7	A30812	sex pheromone cCf1
17	10	32.3	7	A28340	myomodulin - Calif
18	10	32.3	7	ECMUCR	catch-relaxing pep
19	9	29.0	5	C41225	copper resistance
20	9	29.0	5	PT0525	T-cell receptor be
21	9	29.0	5	PT0577	T-cell receptor be
22	9	29.0	5	PT0700	surface protein te
23	9	29.0	5	S69237	T-cell receptor be
24	9	29.0	5	PT0565	T-cell receptor be
25	9	29.0	6	B34835	dnaA protein - Pse
26	9	29.0	6	A43766	28K ubiquitin-immu
27	9	29.0	6	I65546	MHC H2-L antigen -
28	9	29.0	6	PT0518	T-cell receptor be
29	9	29.0	6	PT0662	T-cell receptor be

30 9 29.0 7 2 S25266
31 9 29.0 7 2 PM0150
32 9 29.0 7 2 S78024
33 9 29.0 7 2 E30608
34 9 29.0 7 2 PT0671
35 9 29.0 7 2 EX0008
36 9 29.0 7 2 S66442
37 9 29.0 7 2 S09066
38 9 29.0 7 2 A15398
39 8 25.8 4 2 I61883
40 8 25.8 4 2 I37013
41 8 25.8 4 2 I84439
42 8 25.8 5 2 I39964
43 8 25.8 5 2 I39966
44 8 25.8 5 2 I39965
45 8 25.8 5 2 G44817

ALIGNMENTS

RESULT 1

S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C:Accession: S19630
R:Ochi, K.

Int. J. Syst. Bacteriol. 42, 144-150, 1992

A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete g
A:Reference number: S19630; MUID:92144363; PMID:1736962

A:Accession: S19630

A:Molecule type: protein

A:Residues: 1-7 <OCH>

A:Experimental source: strain IFO 13189

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match 41.9%; Score 13; DB 2; Length 7;

Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKLSR 7

Db |||: 7

RESULT 2

T13892

cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag
C:Species: mitochondrion Lampetra fluviatilis (river lamprey)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: T13892

R:Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.

Mol. Biol. Evol. 14, 807-813, 1997

A:Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI

A:Reference number: Z17775; MUID:97398704; PMID:9254918

A:Accession: T13892

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3 <DE>

A:Cross-references: EMBL:X09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123

C:Genetics:

A:Genome: mitochondrion

C>Note: COI

C:Keywords: mitochondrion; oxidoreductase

Query Match

Best Local Similarity 35.5%; Score 11; DB 3; Length 3;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKL 3

|||

Db 1 MTL 3

RESULT 3

T46627 hypothetical protein c4 - loblolly pine

C:Species: Pinus taeda (loblolly pine)

C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C:Accession: T46627

R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.

submitted to the EMBL Data Library, July 1995

A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do

A:Reference number: Z23105

A:Accession: T46627

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-4 <CHA>

A:Cross-references: EMBL:U31309; NID:G974285; PID:G974292

A:Experimental source: strain s6FTxs6FT3; 8 month seedlings

Query Match 35.5%; Score 11; DB 2; Length 4;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5

Db 1 MKL 3

RESULT 4

E42364 flagellar protein flir - Salmonella typhimurium (fragment)

C:Species: Salmonella typhimurium

C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004

C:Accession: E42364

R:Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.

J. Bacteriol. 173, 3564-3572, 1991

A>Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq

A:Reference number: A42364; MUID:91258342; PMID:1646201

A:Accession: E42364

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-5 <VOG>

A:Cross-references: UNIPROT:P26416; GB:M62408

Query Match 35.5%; Score 11; DB 2; Length 5;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3

Db 2 ITL 4

RESULT 5

I49424

cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49424

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.

Mamm. Genome 5, 349-355, 1994

A>Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: I48934; MUID:94319082; PMID:8043949

A:Accession: I49424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: EMBL:U05745; NID:G497084; PID:NAB60481.1; PID:G642831

C:Keywords: hydrolase; serine proteinase

Query Match 35.5%; Score 11; DB 2; Length 6;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5

Db 3 MKL 5

RESULT 6

JN0859

peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito

C:Species: Sarda orientalis (striped bonito)

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C:Accession: JN0859

R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

BioSci. Biotechnol. Biochem. 57, 1743-1744, 1993

A>Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory p

A:Reference number: JN0859; MUID:94080036; PMID:7764272

A:Accession: JN0859

A:Molecule type: protein

A:Residues: 1-7 <MAT>

A:Experimental source: intestine

C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotens

C:Superfamily: bradykinin-potentiating peptide

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 35.5%; Score 11; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KLSR 7

Db 4 KLEK 7

RESULT 7

A28709

phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)

C:Species: Bacillus cereus

C>Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993

C:Accession: A28709

R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.

Biochemistry 27, 2229-2234, 1988

A>Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence

A:Reference number: A28709; MUID:88241058; PMID:3132206

A:Accession: A28709

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <OLS>

Query Match 35.5%; Score 11; DB 2; Length 7;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5

Db 1 LKI 3

RESULT 8

E48394

glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: E48394

R:Wather, I.H.; Banghart, L.R.; Lane, W.S.

Biochem. Mol. Biol. Int. 29, 545-554, 1993

A>Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-p

II-like sequences.

A:Reference number: A48394; MUID:93250576; PMID:8485470

A:Accession: E48394

A:Status: preliminary

A:Molecule type: protein

A;Residues: 1-7 <MAT>
 A;Experimental source: milk
 A;Note: sequence extracted from NCBI backbone (NCBIP:131450)
 C;Keywords: glycoprotein

Query Match 35.5%; Score 11; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7
 :||
 Db 4 ELAR 7

RESULT 9

I48086
 DNA topoisomerase II alpha - Chinese hamster (fragment)
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C;Accession: I48086
 R;Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
 J. Biol. Chem. 270, 25850-25858, 1995
 A;Title: Molecular cloning and characterization of the promoter for the Chinese hamster
 A;Reference number: I48086; MUID:96029684; PMID:7592770
 A;Accession: I48086
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-7 <RES>
 A;Cross-references: EMBL:U34196; NID:gl041231; PIDN:AA52315.1; PID:gl041232

Query Match 35.5%; Score 11; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKLS 6
 :||
 Db 1 MELS 4

RESULT 10

B48394
 major fat-globule membrane protein GP 55 - guinea pig (fragment)
 C;Species: Cavia porcellus (guinea pig)
 C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C;Accession: B48394
 R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
 Biochem. Mol. Biol. Int. 29, 545-554, 1993
 A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
 II-like sequences.
 A;Reference number: A48394; MUID:93250576; PMID:8485470
 A;Accession: B48394
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-7 <MAT>
 A;Experimental source: milk
 A;Note: sequence extracted from NCBI backbone (NCBIP:131444)

Query Match 35.5%; Score 11; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLSR 7
 :||
 Db 4 ELAR 7

RESULT 11

I40505
 hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
 C;Species: Bacillus stearothermophilus
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
 C;Accession: I40505
 R;Waye, M.W.; Winter, G.

Err. J. Biochem. 158, 505-510, 1986

A;Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA syr
 A;Reference number: I40503; MUID:86274732; PMID:3525162
 A;Accession: I40505
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-4 <RES>
 A;Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:gs80944

Query Match 32.3%; Score 10; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
 :||
 Db 2 LSK 4

RESULT 12

TI4910
 hypothetical protein - parsley
 C;Species: Petroselinum crispum (parsley)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C;Accession: TI4910
 R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, B.; Frohnmeyer, H.
 Mol. Gen. Genet. 257, 595-605, 1998
 A;Title: CRRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
 A;Reference number: Z18261; MUID:98265918; PMID:9604882
 A;Accession: TI4910
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-5 <KIR>
 A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905
 A;Experimental source: ssp. Hamburger Schnitt

Query Match 32.3%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LSR 7
 :||
 Db 2 VSR 4

RESULT 13

I48126
 alpha-tubulin - Chinese hamster (fragment)
 C;Species: Cricetulus griseus (Chinese hamster)
 C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
 C;Accession: I48126
 R;Elliot, E.M.; Sarangi, F.; Henderson, G.; Ling, V.
 Can. J. Biochem. Cell Biol. 63, 511-518, 1985
 A;Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chinese hamster
 A;Reference number: I48126; MUID:86001952; PMID:2931165
 A;Accession: I48126
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-6 <RES>
 A;Cross-references: GB:M25895; NID:g341417; PIDN:AAA74493.1; PID:g516601
 C;Genetics:
 A;Introns: 3/3

Query Match 32.3%; Score 10; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KLS 6
 :||
 Db 2 KLA 4

RESULT 14

B33932

Thu Nov 4 07:26:54 2004

Ig mu chain D region (D23) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
 C;Accession: B33932
 P;Baccala, R.; Vo Quang, T.; Gilbert, M.; TERNYNCK, T.; Avrameas, S.
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
 A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-l
 A;Reference number: A33932; MUID:89282823; PMID:2499887
 A;Accession: B33932
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-6 <BAC>
 A;Cross-references: GB:M27107
 C;Keywords: immunoglobulin

Query Match 32.3%; Score 10; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5
 | : |
 Db 3 LRL 5

RESULT 15

PN0649
 pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
 C;Species: Bacillus sp.
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
 C;Accession: PN0649
 R;Kim, C.H.; Choi, H.I.; Lee, D.S.
 Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
 A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalop
 A;Reference number: PN0649; MUID:94080025; PMID:7764261
 A;Accession: PN0649
 A;Molecule type: protein
 A;Residues: 1-7 <KIM>
 C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of st
 nent in high maltose syrups.
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 32.3%; Score 10; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKLS 6
 | : |
 Db 2 LKMS 5

Search completed: November 4, 2004, 01:24:17
 Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 Seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	13	41.9	7	2	Q95945	Q95945 saccharomyc
2	11	35.5	6	2	P82181	P82181 spinacia ol
3	11	35.5	6	2	P82182	P82182 spinacia ol
4	11	35.5	7	2	Q8GL00	Q8GL00 borrelia bu
5	11	35.5	7	2	Q8JER1	Q8JER1 human immun
6	10	32.3	6	2	P82541	P82541 spinacia ol
7	10	32.3	7	1	CARP MYTED	P10420 mytilus edu
8	10	32.3	7	1	CCF1 ENTFA	P20104 enterococcu
9	10	32.3	7	2	P83530	P83530 lactobacill
10	9	29.0	4	2	Q08433	Q08433 rattus sp.
11	9	29.0	5	1	FARP CHICK	P83308 gallus gall
12	9	29.0	7	1	CHOX_ALCSP	P16101 alcaligenes
13	9	29.0	7	1	UC24_MAIZE	P80630 zea mays (m
14	9	29.0	7	2	Q15897	Q15897 homo sapien
15	9	29.0	7	2	P93233	P93233 lyneopersico
16	9	29.0	7	2	O07354	O07354 synechococc
17	9	29.0	7	2	Q8GL04	Q8GL04 borrelia bu
18	9	29.0	7	2	Q8GL12	Q8GL12 borrelia bu
19	9	29.0	7	2	Q8K3H6	Q8K3H6 rattus norv
20	9	29.0	7	2	Q66205	Q66205 transmissib
21	8	25.8	5	1	B104 LITRU	P82100 litoria rub
22	8	25.8	7	1	FAR5_HIRME	P42564 hirudo medi
23	8	25.8	7	1	GRFP_MOUSE	P99025 mus musculu
24	8	25.8	7	2	Q9C5E3	Q9C5E3 arabidopsis
25	8	25.8	7	2	O34028	O34028 sphingomona
26	8	25.8	7	2	P70804	P70804 azotobacter
27	8	25.8	7	2	Q66113	Q66113 cherry leaf
28	8	25.8	7	2	Q9Y1Q9	Q9Y1Q9 human adeno
29	8	25.8	7	2	Q9Y1R0	Q9Y1R0 human adeno
30	8	25.8	7	2	Q9YVE3	Q9YVE3 human adeno
31	8	25.8	7	2	O42564	O42564 fugu rubrip

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32 7 22.6 3 1 LUXE VIBRI P24272 vibrio fisc
33 7 22.6 5 1 B10A_CITPR P13071 citrobacter
34 7 22.6 5 1 UF01_MOUSE P38639 mus musculu
35 7 22.6 5 2 P83073 P83073 bacillus ce
36 7 22.6 6 1 ACPH_RABIT P21554 oryctolagus
37 7 22.6 6 1 UN06_CLOPA P81351 clostridium
38 7 22.6 6 1 VP19_HHVIK P23210 human herpe
39 7 22.6 7 1 ALL7_CYPDO P82158 cydia pomon
40 7 22.6 7 1 WWA1_ACHFU P35919 achatina fu
41 7 22.6 7 1 WWA2_ACHFU P35920 achatina fu
42 7 22.6 7 1 WWA3_ACHFU P35921 achatina fu
43 7 22.6 7 2 Q28742 Q28742 oryctolagus
44 7 22.6 7 2 P92210 P92210 agropyron c
45 7 22.6 7 2 P92214 P92214 amblyopyrum

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ALIGNMENTS

RESULT 1

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Q95945 PRELIMINARY; PRT; 7 AA.
ID Q95945
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

```

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Query Match 41.9%; Score 13; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 4 KLS 6
Db |||
5 KLS 7

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RESULT 2

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P82181 PRELIMINARY; PRT; 6 AA.
ID P82181
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALWARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;

```

```

Qy      5 LSR 7
      :||
      2 ISR 4

Db

RESULT 4
Q8GL00

Qy      1 LTL 3
      :||
      3 ITL 5

Db

Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```



```

RESULT 6
P82541
ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RA MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28458-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR002222; Ribosomal_S19.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
DR Chloroplast; Ribosomal protein; rRNA-binding.
KW NON TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735AA11C000 CRC64;

Query Match 32.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLK 4
DB 3 SLK 5

RESULT 7
CARP MYTED
ID CARP MYTED STANDARD; PRT; 7 AA.
AC P10430;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
CC PIR: A29342; ECMUCR.

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KW Amidation; Direct protein sequencing; Hormone.
RT MOD RES 7 Leucine amide.
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKL 5
DB 5 LRL 7

RESULT 8
CCFL_ENTFA
ID CCFL_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RA MEDLINE=8908313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Asait J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
DR PIR: A30812; A30812.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3
DB 2 VTL 4

RESULT 9
P83530
ID P83530 PRELIMINARY; PRT; 7 AA.
AC P83530;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

```

Query Match 32.3%; Score 10; DB 2; Length 7;
Best Local Similarity 65.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTL 3
Db 1 VTL 3

RESULT 10
Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koitai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).
DR EMBL; S38336; AA019259.1; -;
DR GO; GO:0016740; P:transferase activity; IEA.
DR TRANSFERASE.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
Db 3 LK 4

RESULT 11
FARP CHICK
ID FARP CHICK STANDARD; PRT; 5 AA.
AC P83308;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRPamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
antibodies to FMRPamide.";
RL Nature 305:328-330 (1983).
CC -!- FUNCTION: May function as a neurotransmitter or modulator.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)
family.
CC GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
DR Amidation; Direct protein sequencing; Neuropeptide.
KW MOD_RES 5 5 Phenylalanine amide.
FT

SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTLK 4
Db 1 LPLR 4

RESULT 12
CHOX ALCSP STANDARD; PRT; 7 AA.
AC P16101; 1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohka-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
oxidase from *Alcaligenes* sp.";
RL J. Biochem. 88:197-203 (1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398;
DR Direct protein sequencing; Oxidoreductase.
KW NON_TER 7 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
Db 6 SR 7

RESULT 13
UC24 MAIZE
ID UC24 MAIZE STANDARD; PRT; 7 AA.
AC P80630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447)
(Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi P., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005 (1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.0, its MW is: 30.0 kDa.
CC Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -;
KW Direct protein sequencing.
FT NON_TER 1 1

FT NON TER 7 7 7 665 MW; 6DC1B5B33DC1B5D0 CRC64;
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TLK 4
|
|
Db 2 TAK 4

RESULT 14

Q15897
ID Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Homo sapiens (clone XP6A11A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON TER 1 1
FT NON TER 7 7
SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LK 4
|
|
Db 3 LK 4

RESULT 15

P93233
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN Name=LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843;
RA Oetliker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.

KW Lyase.
FT NON TER 1 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SR 7
|
|
Db 1 SR 2

Search completed: November 4, 2004, 01:23:17
Job time : 99.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:54:10 ; Search time 92.3333 Seconds
(without alignments)
27.196 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_23Sep04:.*
1: Genesep1980s:.*
2: Genesep1990s:.*
3: Genesep2000s:.*
4: Genesep2001s:.*
5: Genesep2002s:.*
6: Genesep2003as:.*
7: Genesep2003bs:.*
8: Genesep2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	64.5	7	5	ABP66518 Human RSV
2	20	64.5	7	6	ABU69381 Respirato
3	20	64.5	7	7	ADE35876 SYNAGIS a
4	20	64.5	7	8	ADI57038 RSV antib
5	19	61.3	7	2	AAW82699 Haemagglu
6	19	61.3	7	2	AAW42013 Rheumatoi
7	19	61.3	7	2	AAW41889 Rheumatoi
8	19	61.3	7	4	ABBS5870 Vascular
9	19	61.3	7	4	ABBS5283 Vascular
10	19	61.3	7	4	ABBS5981 Vascular
11	19	61.3	7	4	AAU28602 DPI trypt
12	19	61.3	7	4	AAU24969 Schizoph
13	19	61.3	7	4	AAU26249 Depressio
14	19	61.3	7	4	AAU15313 Schizoph
15	19	61.3	7	4	ABBS2355 Human API
16	19	61.3	7	5	ABP66489 Human RSV
17	19	61.3	7	5	ABG78901 Multiple
18	19	61.3	7	5	ABG78730 Multiple
19	19	61.3	7	6	ABP58010 Prostate
20	19	61.3	7	6	ABU69352 Respirato
21	19	61.3	7	6	ABP57255 Breast ca
22	19	61.3	7	6	ABBS9042 Alzheimer
23	19	61.3	7	7	ADE35847 SYNAGIS a
24	19	61.3	7	8	ADH35821 Vitamin D
25	19	61.3	7	8	ADH35827 Vitamin D

ALIGNMENTS

RESULT 1

ABP66518
ID ABP66518 standard; peptide; 7 AA.

XX AC ABP66518;

DT 04-DEC-2002 (first entry)

XX DS Human RSV antibody VL CDR2 fragment.

XX KW Human; variable heavy domain; variable light domain; CDR: VH; VL; RSV;
KW complementarity determining region; respiratory syncytial virus;
KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
KW bronchopulmonary dysplasia; congenital heart disease;
KW congenital immunodeficiency; acquired immunodeficiency.

XX OS Homo sapiens.

XX PN WO200243660-A2.

XX PD 06-JUN-2002.

XX PF 28-NOV-2001; 2001WO-US044807.

XX PR 28-NOV-2000; 2000US-00724396.

XX PR 28-NOV-2000; 2000US-00724531.

XX PA (MEDI-) MEDIUMMUNE INC.

XX PI Young JF, Koenig S, Johnson LS;

XX DR WPI; 2002-706803/76.

XX PT Antibody for treating respiratory syncytial virus (RSV) infection,
PT comprises a variable heavy/light domain or complementarity determining
PT regions 1 3 of variable light/heavy chains, that immunospecifically
PT binds to RSV antigen.

XX PS Claim 8; Page 55; 298pp; English.

XX CC The invention relates to a novel antibody comprising a variable heavy
XX CC (VH) domain, variable light (VL) domain, VH complementarity determining
XX CC region (CDR)-1, VH CDR2, VL CDR1, VL CDR2 or VL CDR3, where the
XX CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX CC and immunostimulant activity. The polynucleotides of the invention may

26 19 61.3 7 8 ADI57009 RSV antib
27 19 61.3 7 8 ADN32134 Human Alz
28 19 61.3 7 8 ADO78580 Schizoph
29 18 58.1 6 5 AAE21359 S. cerevi
30 18 58.1 7 2 AAW82668 Cauliflow
31 18 58.1 7 3 AAB02931 Nucleotid
32 18 58.1 7 4 AAE10492 Humanised
33 18 58.1 7 5 ABP66389 Human RSV
34 18 58.1 7 5 ABP66450 Human RSV
35 18 58.1 7 5 ABP66485 Human RSV
36 18 58.1 7 5 ABP49796 Zinc fing
37 18 58.1 7 5 ABP48455 Zinc fing
38 18 58.1 7 5 ABP51172 Zinc fing
39 18 58.1 7 5 ABP49577 Zinc fing
40 18 58.1 7 5 ABP49790 Zinc fing
41 18 58.1 7 5 ABB07139 Human ery
42 18 58.1 7 5 AAE28044 Human mod
43 18 58.1 7 6 ABU69348 Respirato
44 18 58.1 7 6 ABU69252 Respirato
45 18 58.1 7 6 ABU69313 Respirato

CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a complementary determining region
 CC peptide from a human RSV antibody of the invention
 XX
 SQ Sequence 7 AA;

Query Match 64.5%; Score 20; DB 5; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLS 6
 Db 2 TMKLS 6

RESULT 2
 ID ABU69381 standard; peptide; 7 AA.
 XX
 AC ABU69381;

DT 03-JUN-2003 (first entry)

DE Respiratory syncytial virus (RSV) antibody fragment #126.

XX Respiratory syncytial virus; RSV; vaccine; antibody;
 KW variable heavy domain; VH; variable light domain; VL;
 KW complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection;
 KW cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immune deficiency;
 KW bone marrow transplant.

XX Homo sapiens.

OS US2002177126-A1.

PN 28-NOV-2002.

PD 28-NOV-2001; 2001US-00996288.

PF 28-NOV-2000; 2000US-00724531.

PR (MEDI-) MEDIMMUNE INC.

PI Young JF, Koenig S, Johnson LS;

XX WPI; 2003-340947/32.

DR New antibody comprising a variable heavy (VH) or variable light (VL)
 PT domain or complementarity determining region (CDR), such as CDR1, CDR2,
 PT or CDR3, useful for preventing or treating a respiratory syncytial virus
 PT (RSV) infection.

PS Claim 8; Page 24; 165pp; English.

XX The invention describes an antibody comprising a variable heavy (VH) or
 CC variable light (VL) domain or complementarity determining region (CDR),
 CC such as CDR1, CDR2, or CDR3, which immunospecifically binds to a
 CC respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The
 CC antibody, pharmaceutical compositions and methods are useful for
 CC preventing, treating or ameliorating a RSV infection in patients with
 CC cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease,
 CC congenital immunodeficiency, or acquired immune deficiency, or patients
 CC having had a bone marrow transplant or the elderly. This is the amino
 CC acid sequence of a respiratory syncytial virus (RSV) antibody peptide

XX Sequence 7 AA;

Query Match 64.5%; Score 20; DB 6; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLS 6
 Db 2 TMKLS 6

RESULT 3

AD35876 standard; peptide; 7 AA.

XX ADE35876;

AC ADE35876;

DT 29-JAN-2004 (first entry)

DE SYNAGIS antibody based light chain variable region 2, VL2, CDR #54.
 XX respiratory syncytial virus; RSV infection; high affinity antibody;
 KW high avidity antibody; low antibody dose; more effective prophylaxis;
 KW complementarity determining region; CDR; human.

XX Synthetic.
 OS Homo sapiens.

PN US2003091584-A1.

XX 15-MAY-2003.

PD 28-NOV-2001; 2001US-00996265.

PF 28-NOV-2000; 2000US-00724396.

PR (YOUNG) YOUNG J F.

PA (KOENIG) KOENIG S.

PA (JOHN) JOHNSON L S.

XX Young JF, Koenig S, Johnson LS;

XX WPI; 2003-874589/81.

PT Preventing, treating or ameliorating symptoms associated with respiratory
 PT syncytial virus infection in mammal by administering antibodies or their
 PT fragments that immunospecifically bind to RSV antigens.

PS Claim 111; SEQ ID NO 164; 161pp; English.

XX The invention relates to a method of preventing, treating or ameliorating
 CC one or more symptoms associated with a respiratory syncytial virus (RSV)
 CC infection in a mammal. A sustained release formulation comprising one or
 CC more antibodies or their fragments that immunospecifically bind to one or
 CC more RSV antigens and a pharmaceutical composition comprising one or more
 CC antibodies or their fragments that immunospecifically bind to one or more
 CC RSV antigens formulated for pulmonary delivery is useful for preventing,
 CC treating or ameliorating one or more symptoms associated with a RSV
 CC infection in a mammal by administering the formulation to the mammal, or
 CC the composition to the lungs of the mammal. The antibodies bind to RSV
 CC antigen with a high affinity and/or high avidity. The methods use lower
 CC doses of antibodies which immunospecifically bind to RSV antigen, and
 CC which provide a more effective prophylaxis. The present sequence
 CC represents the amino acid sequence of a complementarity determining
 CC region based on the SYNAGIS antibody.

XX Sequence 7 AA;

Query Match 64.5%; Score 20; DB 7; Length 7;
 Best Local Similarity 80.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLS 6
 Db 2 TMKLS 6

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CC
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RESULT 4
ADI57038
ID ADI57038 standard; peptide; 7 AA.
XX
XX AC ADI57038;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE RSV antibody light chain variable region CDR2 #44.
XX
XX KW human; liquid antibody formulation; antibody;
XX KW respiratory syncytial virus; RSV; RSV infection.
XX
XX OS Homo sapiens.
XX
XX PN WO2003106644-A2.
XX
XX PD 24-DEC-2003.
XX
XX PF 16-JUN-2003; 2003WO-US018914.
XX
XX PR 14-JUN-2002; 2002US-0388920P.
XX
XX PA (MEDI-) MEDIMUNE INC.
XX
XX PI Oliver CN, Allan CB, Chang S;
XX
XX WPI; 2004-082183/08.
XX
XX PT Liquid antibody formulation, useful for treating symptoms associated with
XX PT respiratory syncytial virus (RSV) infection, comprising antibody or its
XX PT fragment binding immunospecifically to RSV antigen and histidine.
XX
XX PS Disclosure; SEQ ID NO 164; 169pp; English.
XX
XX CC The invention relates to a liquid antibody formulation comprising 15 or
XX CC more mg/ml of antibody, or its fragment that immunospecifically binds to
XX CC a respiratory syncytial virus (RSV) antigen and histidine in an aqueous
XX CC carrier. The formulation is useful for preventing, treating or
XX CC ameliorating one or more symptoms associated with a RSV infection in a
XX CC subject, which involves administering a prophylactically or
XX CC therapeutically effective amount of the formulation. The formulation is a
XX CC stable liquid formulation of an anti-RSV antibody effective in preventing
XX CC or treating RSV infection. The present sequence represents the amino acid
XX CC sequence of a RSV antibody light chain variable region CDR2.
XX
SQ Sequence 7 AA;
Query Match 64.5%; Score 20; DB 8; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLKLS 6
Db 2 TWKLS 6
|:|
|:|

RESULT 5
AAW69269
ID AAW69269 standard; peptide; 7 AA.
XX
XX AC AAW69269;
XX
XX DT 29-OCT-1998 (first entry)
XX
XX DE Haemagglutinin heavy chain (HA1) fragment.
XX
XX KW Acryloylated peptide polymer; immune response; peptide epitope;
XX KW synthetic vaccine; enzymatically cleavable site.
XX
XX OS Influenza virus.
```

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CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
SQ

Key Location/Qualifiers
Misc-difference 1 /note= "linked to acryloylated peptide polymer"
WO9834968-A1.
13-AUG-1998.
10-FEB-1998; 98WO-AU000076.
11-FEB-1997; 97AU-00005071.
03-OCT-1997; 97CA-02217321.
(COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
(CSIR ) COMMONWEALTH SCI & IND RES ORG.
(UYME ) UNIV MELBOURNE.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
(CSLC-) CSL LTD.
Jackson DC, O'Brien-Simpson NM, Brown LE, Zeng W, Ede NU;
Brandt ER, Good MF;
WPI; 1998-447177/38.
Acryloylated peptide polymers - useful for synthetic vaccine technology,
for raising an immune response to peptide epitope and as diagnostic tool.
Example 1; Page 20; 77pp; English.
This sequence represents a fragment of the heavy chain (HA1) of the
haemagglutinin of influenza virus. This sequence was used to test the
acryloylated peptide polymer of the invention. The peptide polymers are
used to raise an immune response to a peptide epitope (such as this
sequence), and also as diagnostic tools. Polymers (molecular wt. >600
kDa.) can be prepared with virtually any number of the same or different
epitopes by a method that allows purification of the individual
determinants, avoids errors inherent in long sequential syntheses in
which protected peptide fragments are not used, thus avoiding solubility
and purification problems. Multiple copies of many different peptide
epitopes may be incorporated into a single polymeric structure to allow
utilisation of the range of T cell epitopes required for outbred
populations in conjunction with epitopes representing different
pathogenic serodemes, thus making them a significant advance in synthetic
vaccine technology
XX
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 TLKLS 6
Db 1 TLKLA 5
|:|
|:|

RESULT 6
AA42013
ID AA42013 standard; peptide; 7 AA.
XX
XX AC AA42013;
XX
XX DT 09-DEC-1999 (first entry)
XX
XX DE Rheumatoid arthritis diagnostic protein isoform peptide #164.
XX
XX KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADP; detection;
XX KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
XX KW rheumatoid arthritis diagnostic protein isoform; screening;
XX KW expression reference protein isoform; prognosis.
XX
XX OS Homo sapiens.
```

XX FN WO9947925-A2.
XX
XX PD 23-SEP-1999.
XX PF 15-MAR-1999; 99WO-GB000763.
XX PR 13-MAR-1998; 98GB-00005477.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Parekh RB, Patel TP, Townsend RR;
XX PT WPI; 1999-571871/48.
XX DR Diagnosis of human rheumatoid arthritis by two-dimensional
XX PS electrophoresis.
XX PS Disclosure; Page 21; 157pp; English.
XX CC A method has been developed for the diagnosis of human rheumatoid
XX CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
XX CC dimensional array of features. The method can be used for screening,
XX CC diagnosis and prognosis of RA in a subject or for monitoring the effect
XX CC of an anti-RA drug or therapy administered to a subject. The method
XX CC comprises: (a) analysing a sample of serum or plasma and optionally
XX CC synovial fluid by two-dimensional electrophoresis, to generate a two-
XX CC dimensional array of features; (b) identifying at least one chosen
XX CC feature whose relative abundance correlates with the presence or absence
XX CC of RA; and (c) comparing the abundance of each chosen feature in the
XX CC sample with the abundance of that chosen feature in serum or plasma from
XX CC one or more persons without RA, where the relative abundance of the
XX CC chosen feature or features in the sample indicates the presence or
XX CC absence of RA in the subject. The method can also be used in clinical
XX CC studies for testing drugs for therapy of RA, for purification of RA-
XX CC diagnostic protein isoforms (RPIs), and for production of antibodies to
XX CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
XX CC compounds that promote or inhibit their activity, which are then used as
XX CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
XX CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
XX CC AAY42103 represent expression reference protein isoform peptides and
XX CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
XX CC used in the exemplification of the present invention
XX SQ
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TIMISR 7
RESULT 7
AAY41889
ID AAY41889 standard; peptide; 7 AA.
XX AC AAY41889;
XX DT 09-DEC-1999 (first entry)
XX DE Rheumatoid arthritis diagnostic protein isoform peptide #40.
XX KW Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
XX KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
XX KW rheumatoid arthritis diagnostic protein isoform; screening;
XX KW expression reference protein isoform; prognosis.
XX OS Homo sapiens.
XX OS WO9947925-A2.
XX PN

XX PD 23-SEP-1999.
XX PF 15-MAR-1999; 99WO-GB000763.
XX PR 13-MAR-1998; 98GB-00005477.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Parekh RB, Patel TP, Townsend RR;
XX PT WPI; 1999-571871/48.
XX DR Diagnosis of human rheumatoid arthritis by two-dimensional
XX PS electrophoresis.
XX PS Disclosure; Page 18; 157pp; English.
XX CC A method has been developed for the diagnosis of human rheumatoid
XX CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
XX CC dimensional array of features. The method can be used for screening,
XX CC diagnosis and prognosis of RA in a subject or for monitoring the effect
XX CC of an anti-RA drug or therapy administered to a subject. The method
XX CC comprises: (a) analysing a sample of serum or plasma and optionally
XX CC synovial fluid by two-dimensional electrophoresis, to generate a two-
XX CC dimensional array of features; (b) identifying at least one chosen
XX CC feature whose relative abundance correlates with the presence or absence
XX CC of RA; and (c) comparing the abundance of each chosen feature in the
XX CC sample with the abundance of that chosen feature in serum or plasma from
XX CC one or more persons without RA, where the relative abundance of the
XX CC chosen feature or features in the sample indicates the presence or
XX CC absence of RA in the subject. The method can also be used in clinical
XX CC studies for testing drugs for therapy of RA, for purification of RA-
XX CC diagnostic protein isoforms (RPIs), and for production of antibodies to
XX CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
XX CC compounds that promote or inhibit their activity, which are then used as
XX CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
XX CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
XX CC AAY42103 represent expression reference protein isoform peptides and
XX CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
XX CC used in the exemplification of the present invention
XX SQ
SQ Sequence 7 AA;
Query Match 61.3%; Score 19; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 TLKLSR 7
Db 2 TFELSR 7
RESULT 8
ABB55870
ID ABB55870 standard; peptide; 7 AA.
XX AC ABB55870;
XX DT 15-FEB-2002 (first entry)
XX DE Vascular dementia-associated protein isoform (VPI) 70.
XX KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX KW diagnosis; prognosis; gene therapy.
XX OS Homo sapiens.
XX PN WO200169261-A2.
XX PD 20-SEP-2001.
XX PF 14-MAR-2001; 2001WO-GB001106.

[illegible]

CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB5801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy

XX Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1;

QY 2 TLKLSR 7
 DB 2 TFEISR 7

RESULT 11
 AAU28602
 ID AAU28602 standard; peptide; 7 AA.

XX AAU28602;

03-JAN-2002 (first entry)
 DPI tryptic digest peptide #199.

XX Human; depression associated protein isoform; tryptic digest peptide;
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
 KW manic-depressive illness; schizoaffective disorder.

XX Homo sapiens.

PN WO200162787-A1.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB000786.

XX 24-FEB-2000; 2000GB-00004412.

PR 08-DEC-2000; 2000GB-00030050.

PR 12-DEC-2000; 2000US-0254830P.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570626/64.

XX Novel nucleic acid encoding a protein associated with bipolar affective

PT disorder, which is used for diagnosis, prophylaxis and therapy of

PT neuropsychiatric disorders, such as bipolar affective disorder.

XX Disclosure; Page 34; 153pp; English.

XX The present invention relates to the identification of depression
 CC associated protein isoforms (DPIs), particularly the tryptic digest
 CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar
 CC affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are
 CC increased in BAD subjects. Also described are peptide sequences
 CC identified from DPI-45 and DPI-213 and the nucleic acid sequence they are
 CC encoded by. The sequences of the invention are useful for clinical

CC screening, diagnosis, prognosis, therapy and prophylaxis of
 CC neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder,
 CC BP), manic-depressive illnesses, attention deficit disorders,
 CC schizoaffective disorders, and unipolar affective disorders. The present
 CC sequence represents one of the DPI tryptic digest peptides of the present
 CC invention

XX Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1;

QY 2 TLKLSR 7
 DB 2 TFEISR 7

RESULT 12
 AAU24969
 ID AAU24969 standard; peptide; 7 AA.

XX AAU24969;

18-DEC-2001 (first entry)

XX Schizophrenia-Associated Protein Isoform (SPI) peptide #198.

XX Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
 KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX Homo sapiens.

PN WO200162785-A2.

XX 30-AUG-2001.

XX 23-FEB-2001; 2001WO-GB000792.

PR 24-FEB-2000; 2000GB-00004415.

PR 28-DEC-2000; 2000US-00750395.

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;

XX WPI; 2001-570624/64.

XX New schizophrenia associated protein isoforms and encoding nucleic acid
 PT molecules, useful for treatment, diagnosis and prognosis of schizophrenia
 PT and screening for potential drugs for treatment and new drug targets.

XX Disclosure; Page 32; 148pp; English.

XX The sequence represents a schizophrenia-associated protein isoform (SPI).
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable
 CC in cerebrospinal fluid, serum or plasma and are useful markers of
 CC schizophrenia. The sequences can be used for treatment and diagnosis of
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,
 CC identifying patients most likely to respond to a particular therapy and
 CC identification of new targets for drug treatment. SPI DNA is useful as a
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs

XX Sequence 7 AA;

Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1;

QY 2 TLKLSR 7
 DB 2 TFEISR 7

RESULT 13
 AAU26249
 ID AAU26249 standard; peptide; 7 AA.
 XX AC
 XX AAU26249;
 XX
 DT 18-DEC-2001 (first entry)
 XX AC
 XX Depression-Associated Protein isoform DPI-208.
 DE
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 KW CSF; antidepressant; anitmanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 KW unipolar affective disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200163294-A2.
 PN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB000791.
 PF
 XX 24-FEB-2000; 2000GB-00004412.
 PR
 XX 08-DEC-2000; 2000GB-00030050.
 PR
 XX 12-DEC-2000; 2000US-0254830P.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI
 XX WPI; 2001-582081/65.
 DR
 XX
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 PT unipolar depression, or for screening for modulators, comprises a BAD-
 PT associated protein isoform.
 XX
 PS Claim 8; Page 34; 163pp; English.
 XX
 CC The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances. The
 CC present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
 CC subjects having BAD
 XX
 SQ Sequence 7 AA;
 Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TLKLSR 7
 Db | : |||
 2 TFEISR 7
 RESULT 14
 AAU15313
 ID AAU15313 standard; peptide; 7 AA.
 XX AC

XX AAU15313;
 AC
 XX 24-OCT-2001 (first entry)
 DT
 XX Schizophrenia-associated isoform peptide #198.
 DE
 XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW neurological disorder; neuropathy.
 KW
 XX Homo sapiens.
 OS
 XX WO200163293-A2.
 PN
 XX 30-AUG-2001.
 PD
 XX 23-FEB-2001; 2001WO-GB000783.
 PF
 XX 24-FEB-2000; 2000GB-00004415.
 PR
 XX 28-DEC-2000; 2000US-00750395.
 XX
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Herath HMAC, Parekh RB, Rohlf C;
 PI
 XX WPI; 2001-502868/55.
 DR
 XX
 XX Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid.
 XX
 PS Claim 6; Page 32; 160pp; English.
 XX
 CC The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH
 CC Associated Protein Isoforms (SPis) in samples, e.g. by electrophoresis,
 CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SFS, SPis and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neuralgic defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and characterisation of
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU1514-
 CC AAU15762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention
 XX
 SQ Sequence 7 AA;
 Query Match 61.3%; Score 19; DB 4; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 TLKLSR 7
 Db | : |||
 2 TFEISR 7
 RESULT 15
 ABB52355
 ID ABB52355 standard; peptide; 7 AA.
 XX AC ABB52355;

Thu Nov 4 07:26:52 2004

XX 08-FEB-2002 (first entry)
DT Human API-125 tryptic digest peptide #8.
XX
DE
XX
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX
OS Homo sapiens.
XX WO200175454-A2.
FN
XX
XX 11-OCT-2001.
PD
XX
XX 03-APR-2001; 2001WO-US010908.
EF
XX
XX 03-APR-2000; 2000US-0194504P.
FR
PR 28-NOV-2000; 2000US-0253647P.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
XX Durham KL, Friedmann DL, Herath HM, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
XX WPI; 2001-639384/73.
DR
XX
XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
XX Example; Page 34; 162pp; English.
PS
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
XX Sequence 7 AA;
SQ

Query Match 61.3%; Score 19; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 2 TPELSR 7

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JOB time : 94.3333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 Seconds
(without alignments)
32.733 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 56143

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	64.5	7	9	US-09-996-288-164
2	20	64.5	7	10	US-09-996-265-164
3	20	64.5	7	15	US-10-461-863-164
4	19	61.3	7	9	US-09-996-288-164
5	19	61.3	7	9	US-09-996-288-164
6	19	61.3	7	9	US-09-996-288-164
7	19	61.3	7	9	US-09-996-288-164
8	19	61.3	7	10	US-09-996-288-164
9	19	61.3	7	10	US-09-996-288-164
10	19	61.3	7	10	US-09-996-288-164
11	19	61.3	7	11	US-09-996-288-164
12	19	61.3	7	13	US-10-044-034-13
13	19	61.3	7	15	US-10-461-863-135

14	19	61.3	7	15	US-10-264-309-460	Sequence 460, App
15	19	61.3	7	15	US-10-601-100-105	Sequence 105, App
16	19	61.3	7	17	US-10-700-340-154	Sequence 154, App
17	18	58.1	6	9	US-09-897-107-24	Sequence 24, Appl
18	18	58.1	7	9	US-09-989-789-396	Sequence 396, App
19	18	58.1	7	9	US-09-989-789-1971	Sequence 1971, App
20	18	58.1	7	9	US-09-989-789-3503	Sequence 3503, App
21	18	58.1	7	9	US-09-989-789-3542	Sequence 3542, App
22	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
23	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
24	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
25	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
26	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
27	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
28	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
29	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
30	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
31	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
32	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
33	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
34	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
35	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
36	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
37	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
38	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
39	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
40	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
41	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
42	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
43	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
44	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App
45	18	58.1	7	9	US-09-989-789-3544	Sequence 3544, App

ALIGNMENTS

RESULT 1
US-09-996-288-164
; Sequence 164, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-164

Query Match 64.5%; Score 20; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
|:|:|
Db 2 TWKLS 6

RESULT 2
US-09-996-265-164
; Sequence 164, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James

```
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-164

Query Match      64.5%; Score 20; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLS 6
   |::||
Db 2 TMKLS 6

RESULT 3
US-10-461-863-164
; Sequence 164, Application US/10461863
; Publication No. US20040018200A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, Cynthia
; APPLICANT: Allan, Christian
; APPLICANT: Chang, Stephen
; TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMULATIONS
; FILE REFERENCE: 10271-071-999
; CURRENT APPLICATION NUMBER: US/10/461,863
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/388,920
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-461-863-164

Query Match      64.5%; Score 20; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLS 6
   |::||
Db 2 TMKLS 6

RESULT 4
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match      61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
   |::||
Db 2 TFELSR 7

RESULT 5
US-09-938-909-7
; Sequence 7, Application US/09998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John
; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: MTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-909-7

Query Match      61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
   |::||
Db 2 TFELSR 7

RESULT 6
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

Query Match 61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
| : |||
Db 2 TPELSR 7

RESULT 7

US-09-996-288-135
; Sequence 135, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-135

Query Match 61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6
| : |||
Db 2 TLKLA 6

RESULT 8

US-09-791-393-145
; Sequence 145, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

Query Match 61.3%; Score 19; DB 10; Length 7;

Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
| : |||
Db 2 TPELSR 7

RESULT 9

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlff, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145

Query Match 61.3%; Score 19; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKLSR 7
| : |||
Db 2 TPELSR 7

RESULT 10

US-09-996-265-135
; Sequence 135, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylax
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-135

Query Match 61.3%; Score 19; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLS 6

; Sequence 135, Application US/10461863
; Publication No. US20040018200A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, Cynthia
; APPLICANT: Allan, Christian
; APPLICANT: Chang, Stephen
; TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMULI
; FILE REFERENCE: 10271-071-999
; CURRENT APPLICATION NUMBER: US/10/461,863
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/388,920
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-461-863-135

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 6
Db 2 TLKLA 6

RESULT 14
US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHERYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR.
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 460
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 TLKLS 7
Db 2 TFEISR 7

; Sequence 135, Application US/10461863
; Publication No. US20040018200A1
; GENERAL INFORMATION:
; APPLICANT: Oliver, Cynthia
; APPLICANT: Allan, Christian
; APPLICANT: Chang, Stephen
; TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMULI
; FILE REFERENCE: 10271-071-999
; CURRENT APPLICATION NUMBER: US/10/461,863
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: 60/388,920
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-461-863-135

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7

Query Match 61.3%; Score 19; DB 11; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 TLKLSR 7
Db 2 TFEISR 7


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RESULT 15
US-10-601-100-105
; Sequence 105, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; TITLE OF INVENTION: Neurological Diseases
; FILE REFERENCE: 11362.0038.NPUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105

Query Match      61.3%; Score 19; DB 15; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 TLKLSR 7
      | :|||
Db      2 TFELSR 7

Search completed: November 4, 2004, 01:43:17
Job time : 69.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	93.5	113	3	US-08-983-607-25
2	28	90.3	474	4	US-08-081-385-148
3	27	87.1	127	1	US-08-482-882-45
4	27	87.1	127	2	US-08-483-389-45
5	27	87.1	127	2	US-08-487-113D-45
6	27	87.1	127	2	US-08-473-503-45
7	27	87.1	127	2	US-08-483-932-45
8	27	87.1	127	2	US-08-720-420A-45
9	27	87.1	127	3	US-08-714-017-45
10	27	87.1	127	3	US-08-475-680-45
11	27	87.1	133	4	US-09-472-087-26
12	27	87.1	133	4	US-09-472-087-116
13	27	87.1	141	3	US-09-134-001C-3710
14	27	87.1	221	4	US-09-352-991A-17454
15	27	87.1	229	4	US-09-198-452A-366
16	27	87.1	446	4	US-09-248-796A-15638
17	27	87.1	551	4	US-09-538-092-738
18	27	87.1	649	3	US-09-066-047-5
19	26	83.9	70	4	US-09-543-681A-7976
20	26	83.9	172	4	US-09-248-796A-22198
21	26	83.9	222	4	US-09-543-681A-5317
22	26	83.9	359	3	US-09-134-001C-5618
23	26	83.9	398	4	US-10-037-616-26
24	26	83.9	399	4	US-09-328-352-7463
25	26	83.9	411	4	US-09-270-767-45365
26	26	83.9	529	4	US-09-270-767-43463
27	26	83.9	695	4	US-09-543-681A-7766

28 25 80.6 32 1 US-08-477-877B-33
29 25 80.6 32 1 US-07-977-696C-71
30 25 80.6 32 1 US-08-129-930B-71
31 25 80.6 32 2 US-08-472-281A-33
32 25 80.6 32 2 US-08-477-989B-33
33 25 80.6 32 3 US-08-976-288A-71
34 25 80.6 32 4 US-09-563-222C-80
35 25 80.6 32 4 US-09-563-222C-114
36 25 80.6 61 4 US-09-621-976-6215
37 25 80.6 67 4 US-09-248-796A-18940
38 25 80.6 69 4 US-09-270-767-39121
39 25 80.6 69 4 US-09-270-767-54338
40 25 80.6 81 1 US-08-497-312-19
41 25 80.6 81 4 US-09-254-180C-154
42 25 80.6 81 4 US-09-254-180C-155
43 25 80.6 81 4 US-09-254-180C-156
44 25 80.6 81 4 US-09-254-180C-157
45 25 80.6 81 4 US-09-254-180C-158

ALIGNMENTS

RESULT 1
US-08-983-607-25
; Sequence 25, Application US/08983607
; Patent No. 6140470
; GENERAL INFORMATION:
; APPLICANT: Alan Garen
; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; TITLE OF INVENTION: Bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; ADDRESSEE: and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes

IMMEDIATE SOURCE:
LIBRARY: DM414 scfv antibodies obtained from
LIBRARY: FUSE5 fusion phage construct
CLONE: D33
FEATURE:
NAME/KEY: light chain
OTHER INFORMATION: Xaa at position 47 is His or
OTHER INFORMATION: Gly and Xaa at position 95 is His or Gln
US-08-983-607-25

Query Match 93.5%; Score 29; DB 3; Length 113;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 76 LTLKLSR 82

RESULT 2
US-09-081-385-148
Sequence 148, Application US/09081385
Patent No. 6593456
GENERAL INFORMATION:
APPLICANT: Gatanaga, T.
TITLE OF INVENTION: Factors Altering Tumor Necrosis
TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
TITLE OF INVENTION: of Use Thereof
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,385
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/964,747
FILING DATE: 05-NOV-1997
APPLICATION NUMBER: 60/030,761
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wu, Frank
REGISTRATION NUMBER: 41,385
REFERENCE/DOCKET NUMBER: 22000-20577.21
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-081-385-148

Query Match 90.3%; Score 28; DB 4; Length 474;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 358 LTLKLSR 364

RESULT 3
US-08-482-882-45
Sequence 45, Application US/08482882
Patent No. 5773218
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and Methods
NUMBER OF SEQUENCES: 116
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,882
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
FILING DATE:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5773218and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-482-882-45

Query Match 87.1%; Score 27; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 4

US-08-483-389-45
 ; Sequence 45, Application US/08483389
 ; Patent No. 5811517
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Vazeux, Rosemay
 ; TITLE OF INVENTION: ICAM-RELATED PROTEIN
 ; NUMBER OF SEQUENCES: 118
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive/6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,389
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/894,061
 ; FILING DATE: 05-JUN-1992
 ; APPLICATION NUMBER: US 07/889,724
 ; FILING DATE: 26-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,689
 ; FILING DATE: 27-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Suh, Young J.
 ; REGISTRATION NUMBER: P-41,337
 ; REFERENCE/DOCKET NUMBER: 27866/32760
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: (312) 474-6600
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-389-45

Query Match 87.1%; Score 27; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
 Db 92 TLKLSR 97

RESULT 5
 US-08-487-113D-45
 ; Sequence 45, Application US/08487113D
 ; Patent No. 5837822
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Vazeux, Rosemay
 ; TITLE OF INVENTION: ICAM-Related Materials and Methods
 ; NUMBER OF SEQUENCES: 120

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,113D
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286,754
 ; FILING DATE: 05-AUG-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/102,852
 ; FILING DATE: 05-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/009,266
 ; FILING DATE: 22-JAN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/894,061
 ; FILING DATE: 05-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/889,724
 ; FILING DATE: 26-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/827,689
 ; FILING DATE: 27-JAN-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5837822and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 32744
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 45:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 127 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-487-113D-45

Query Match 87.1%; Score 27; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
 Db 92 TLKLSR 97

RESULT 6
 US-08-473-503-45
 ; Sequence 45, Application US/08473503
 ; Patent No. 5869262
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallatin, W. Michael
 ; APPLICANT: Vazeux, Rosemay
 ; TITLE OF INVENTION: ICAM-Related Materials and Methods
 ; NUMBER OF SEQUENCES: 116
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 S. Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois

us-09-712-819d-13.open.ra1

Thu Nov 4 07:26:55 2004

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;
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 586926and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-473-503-45

Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 7
US-08-483-932-45
; Sequence 45, Application US/08483932
; Patent No. 5880268
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,503
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 586926and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-932-45

Query Match 87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 8
US-08-720-420A-45
; Sequence 45, Application US/08720420A
; Patent No. 5989843
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,420A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/487,113
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Joseph A., Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 33282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-720-420A-45

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Query Match      87.1%; Score 27; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 TLKLSR 7
Db      92 TLKLSR 97

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RESULT 9
US-08-714-017-45
; Sequence 45, Application US/08714017
; Patent No. 6040176
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE:

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; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6040176and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 127 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-714-017-45

```

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Query Match      87.1%; Score 27; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 TLKLSR 7
Db      92 TLKLSR 97

```

```

RESULT 10
US-08-475-680-45
; Sequence 45, Application US/08475680
; Patent No. 6100383
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 116
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,680
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/286,754
; FILING DATE: 05-AUG-1994
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:

```

APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 116
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-116

Query Match 87.1%; Score 27; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 63 TLKLSR 68

RESULT 13
US-09-134-001C-3710
Sequence 3710, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3710
LENGTH: 141
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3710

Query Match 87.1%; Score 27; DB 3; Length 141;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 53 LTLKLSR 59

RESULT 14
US-09-252-991A-17454
Sequence 17454, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

APPLICATION NUMBER: US 07/894,061
FILING DATE: 05-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100383and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32178
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-680-45

Query Match 87.1%; Score 27; DB 3; Length 127;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 92 TLKLSR 97

RESULT 11
US-09-472-087-26
Sequence 26, Application US/09472087
Patent No. 6682736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-26

Query Match 87.1%; Score 27; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLKLSR 7
Db 63 TLKLSR 68

RESULT 12
US-09-472-087-116
Sequence 116, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17454
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17454

Query Match 87.1%; Score 27; DB 4; Length 221;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LTKLSR 7
|||
Db 161 LTFKLSR 167

RESULT 15
US-09-198-452A-366
; Sequence 366, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 366
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-366

Query Match 87.1%; Score 27; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKLSR 7
|||
Db 247 TLKLSR 252

Search completed: November 4, 2004, 00:54:52
Job time : 16.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:36:19 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTLKLSR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	203	2 C64038	hypothetical prote
2	31	100.0	382	2 T19701	phosphoprotein pho
3	29	93.5	555	2 C71414	hypothetical prote
4	29	93.5	726	2 T33998	hypothetical prote
5	28	90.3	153	2 AB1174	hypothetical prote
6	28	90.3	153	2 AF1531	hypothetical prote
7	28	90.3	633	2 AE2591	DNAK protein limpo
8	28	90.3	633	2 E97373	dnaJ protein (heat
9	28	90.3	686	2 C83734	beta-hexosamidase
10	28	90.3	845	2 G82773	phage-related prot
11	27	87.1	139	2 T30212	probable transcrip
12	27	87.1	139	2 B89874	hypothetical prote
13	27	87.1	189	2 A83573	conserved hypotet
14	27	87.1	191	2 B86937	hypothetical prote
15	27	87.1	259	2 B72089	hypothetical prote
16	27	87.1	259	2 B86534	ABC transporter, A
17	27	87.1	259	2 G81714	ABC transporter, A
18	27	87.1	259	2 F71561	probable rRNA meth
19	27	87.1	284	2 H82675	conserved hypotet
20	27	87.1	336	1 R5WX10	ribosomal protein
21	27	87.1	360	2 T17996	hypothetical prote
22	27	87.1	389	1 F64426	phosphate-binding
23	27	87.1	428	2 G86247	protein T23J18.5 [
24	27	87.1	551	2 S60994	VPS17 protein - ye
25	27	87.1	645	2 T45482	heat shock protein
26	26	83.9	108	2 T17725	hypothetical prote
27	26	83.9	151	1 GGGACR	globin - horn shel
28	26	83.9	187	2 AF0255	probable phage pro
29	26	83.9	198	2 AB1598	conserved hypotet

ALIGNMENTS

RESULT 1

C64038

hypothetical protein HI1605 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C/Accession: C64038

R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.H.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64038

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-203 <TIGR>

A:Cross-references: UNIPROT:P44272; GB:U32834; GB:I42023; NID:gl574444; PIDN:AAC23249.1

C:Superfamily: hypothetical protein HI1605

Query Match 100.0%; Score 31; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7

Db 103 LTLKLSR 109

RESULT 2

T19701

phosphoprotein phosphatase (EC 3.1.3.16) C34C12.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004

C/Accession: T19701

R/Kershaw, J. submitted to the EMBL Data Library, December 1994

A:Reference number: Z19166

A:Accession: T19701

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-382 <WIL>

A:Cross-references: EMBL:Z46996; PIDN:CAA87100.1; GSPDB:GN00021; CESP:C34C12.3

A:Experimental source: clone C34C12

C:Genetics:

A:Gene: CESP:C34C12.3

A:Map position: 3

A:Introns: 77/2; 107/2; 145/1; 179/2; 221/3; 265/3; 292/3; 336/1

C:Superfamily: Serine/threonine protein phosphatase; phosphoesterase core homology; phosphoesterase core homology; phosphoesterase core homology

C:Keywords: iron; metalloprotein; phosphoric monoester hydrolase; serine/threonine-spec

F:96-356/Domain: phosphoprotein phosphatase homology <PPP>

F:124-192/Domain: phosphoesterase core homology <PEC>

F;130,132,158/Binding site: iron (Asp, His, Asp) #status predicted
F;158,190,240,315/Binding site: zinc (Asp, Asn, His, His) #status predicted
F;161,191,339/Active site: Asp, His, Tyr #status predicted
F;162,268/Binding site: substrate phosphate (Arg) #status predicted

Query Match 100.0%; Score 31; DB 1; Length 382;

Best Local Similarity 100.0%; Pred. No. 12; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0;

QY 1 LTLKLSR 7
|||||

Db 73 LTLKLSR 79

RESULT 3

C71414

hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: Columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C;Accession: C71414

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ana
C.; Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: C71414

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-555 <BEV>

A;Cross-references: UNIPROT:Q23360; GB:Z97337; NID:G2244829; PID:e326846; PID:G2244863

C;Genetics:

A;Map position: 4COP9-4G3845

Query Match 93.5%; Score 29; DB 2; Length 555;

Best Local Similarity 85.7%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||

Db 411 LTLKLSR 417

RESULT 4

T33998

hypothetical protein W03G1.6 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 16-Aug-2004

C;Accession: T33998

R;Pauley, A.; Scheet, P.; Harper, M.

submitted to the EMBL Data Library, February 1999

A;Description: The sequence of C. elegans cosmid W03G1.

A;Reference number: Z21454

A;Accession: T33998

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-726 <PAU>

A;Cross-references: UNIPROT:Q9UAY1; EMBL:AF125964; PIDN:AADI4754.1; GSPDB:GN00022; CESP:

A;Experimental source: strain Bristol N2; clone W03G1

C;Genetics:

A;Gene: CBSP.W03G1.6

A;Map position: 4

A;Introns: 21/1; 48/3; 87/3; 224/3; 280/3; 347/3; 468/3; 523/1; 584/1; 697/3

C;Superfamily: protein kinase homology

Query Match 93.5%; Score 29; DB 2; Length 726;

Best Local Similarity 85.7%; Pred. No. 67;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||

Db 512 LTLKLSR 518

RESULT 5

AE1174

hypothetical protein lmc0797 [imported] - Listeria monocytogenes (strain EGD-e)

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AE1174

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1174

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-153 <GLA>

A;Cross-references: UNIPROT:Q8Y8U5; GB:NC_003210; PIDN:CAC98875.1; PID:g16410186; GSPDB:

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmc0797

Query Match 90.3%; Score 28; DB 2; Length 153;

Best Local Similarity 85.7%; Pred. No. 26;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||

Db 98 LTLKLSK 104

RESULT 6

AF1531

hypothetical protein lin0790 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AF1531

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-153 <GLA>

A;Cross-references: UNIPROT:Q92DM3; GB:AL592022; PIDN:CAC96022.1; PID:g16413241; GSPDB:

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin0790

Query Match 90.3%; Score 28; DB 2; Length 153;

Best Local Similarity 85.7%; Pred. No. 26;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||

Db 98 LTLKLSK 104

RESULT 7

AE2591

DNAK Protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2591
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, F.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <KUR>
A;Cross-references: UNIPROT:P50019; GB:AE008688; PIDN:AAL41147.1; PID:gl7738443; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: dnaX
A;Map position: circular chromosome
C;Superfamily: heat shock protein 70

Query Match 90.3%; Score 28; DB 2; Length 633;
Best Local Similarity 85.7%; Pred. NO. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 291 LTLKLSR 297

RESULT 8
E97373
dnaJ protein (heat shock protein 70) (hsp70) [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: E97373
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: E97373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <KUR>
A;Cross-references: UNIPROT:P50019; GB:AE007869; PIDN:AAK35942.1; PID:gl5154995; GSPDB:G
C;Genetics:
A;Gene: AGR_C_195
A;Map position: circular chromosome
C;Superfamily: heat shock protein 70

Query Match 90.3%; Score 28; DB 2; Length 633;
Best Local Similarity 85.7%; Pred. NO. 1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 291 LTLKLSR 297

RESULT 9
C83734
beta-hexosaminidase A precursor BH0675 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83734
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83734
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-686 <STO>
A;Cross-references: UNIPROT:Q9KF22; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA504
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0675

Query Match 90.3%; Score 28; DB 2; Length 686;
Best Local Similarity 85.7%; Pred. NO. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 471 LTLKLSR 477

RESULT 10
G82773
phage-related protein XF0705 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82773
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82773
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-845 <SIM>
A;Cross-references: UNIPROT:Q9PFF4; GB:AE003913; GB:AE003849; NID:99105578; PIDN:AAF835
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; A
Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrier, M
as-Neto, B.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, J.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savas
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silve
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
A;Reference number: A59328
A;Accession: G82773
A;Contents: annotation
C;Genetics:
A;Gene: XF0705

Query Match 90.3%; Score 28; DB 2; Length 845;
Best Local Similarity 85.7%; Pred. NO. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
|||||
Db 410 LTLKLSR 416

RESULT 11
T30212
probable transcription regulator - Staphylococcus epidermidis
C;Species: Staphylococcus epidermidis
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30212
R;Heilmann, C.; Hussain, M.; Peters, G.; Gotz, F.
Mol. Microbiol. 24, 1013-1024, 1997
A;Title: Evidence for autolysin-mediated primary attachment of Staphylococcus epidermid
A;Reference number: Z20779; MUID:97363715; PMID:9220008
A;Accession: T30212
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-139 <HEI>
A;Cross-references: UNIPROT:Q33636; EMBL:U71377; NID:92267238; PID:92267243; PIDN:AAB639

Query Match	87.1%;	Score 27;	DB 2;	Length 139;
Best Local Similarity	71.4%;	Pred. No. 41;		
Matches	5;	Conservative	2;	Mismatches 0;
		Indels	0;	Gaps 0;

RESULT 12
 B99874
 hypothetical protein SA0904 [imported] - Staphylococcus aureus (strain N315)
 C/Species: Staphylococcus aureus
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C/Accession: B99874
 R/Ruroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A/Reference number: A89758; MUID:21311952; PMID:11418146
 A/Accession: B99874
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-139 <KUR>
 A/Cross-references: UNIPROT:Q93V42; GB:BA000018; PFD:gl3700853; PFDN:BA842149.1; GSPDB:G
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: SA0904

Query Match 87.1%; Score 27; DB 2; Length 139;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 5; Conservative 2; Mismatches 0; Indels

RESULT 13
A83573 conserved hypothetical protein PA0581 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: A83573
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Ez-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: A83573
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-189 <STO>
A:Cross-references: UNIPROT:Q915V6; GB:AE004494; GB:AE004091; NID:g9946446; PIDN:AA00397
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0581
C:Superfamily: *Escherichia coli* *vgH* protein

Query Match	87.1%	Score 27;	DB 2;	Length 189;
Best Local Similarity	85.7%;	Pred. No. 56;		
Matches	6;	Conservative	0;	Mismatches
			1;	Indels
			0;	Gaps
			0;	

RESULT 14
B86937

hypothetical protein folk [imported] - Mycobacterium leprae
C/Species: Mycobacterium leprae
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: B86937
R/Cole, S. T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
A/Title: Massive gene decay in the leprosy bacillus.
A/Reference number: A86909; MUID:21128732; PMID:11234002
A/Accession: B86937
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-191 <STO>
A/Cross-references: UNIPROT:O69528; GB:AL450380; NID:gl3092570; PIDN:CAC29734.1; GSPDB:
C/Genetics:
A/Gen: folk
C/Superfamily: 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase; 2-a

Query Match	87.1%	Score 27;	DB 2;	Length 191;
Best Local Similarity	85.7%;	Pred. No. 56;		
Matches	6;	Mismatches	0;	Gaps 0;
Conservative	6;	Indels	1;	

RESULT 15
B72089
ABC transporter, ATP-binding protein CP0412 [imported] - Chlamydoiphila pneumoniae (str
N:Alternate names: rRNA methylase
C:Species: Chlamydoiphila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 16-Aug-2004
C:Accession: B72089; H81580
R:Kalan, S.; Mitchell, W.; Marxthe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:95206606; PMID:10192388

```
Query Match      87.1%; Score 27; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
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Search completed: November 4, 2004, 00:48:42
Job time : 20 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:41:09 ; Search time 103 Seconds
(without alignments)
39.103 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	203	1 YGIM HAEIN	P42722 rhizobium
2	29	93.5	367	2 Q986H5	Q986H5 rhizobium
3	29	93.5	459	2 Q6N126	Q6N126 corynebacte
4	29	93.5	459	2 CAE49472	CAE49472 corynebacte
5	29	93.5	465	2 Q7NT21	Q7NT21 chromobacte
6	29	93.5	526	2 Q9LG01	Q9LG01 arabidopsis
7	29	93.5	555	2 Q23360	Q23360 arabidopsis
8	29	93.5	636	2 Q74H59	Q74H59 geobacter s
9	29	93.5	636	2 AAR33368	AAR33368 geobacter s
10	29	93.5	641	1 DNAK RHIME	P42374 rhizobium m
11	29	93.5	679	2 Q7SPB7	Q7SPB7 neurospora
12	29	93.5	722	2 Q86PW0	Q86PW0 caenorhabdi
13	29	93.5	726	2 Q9UAY1	Q9UAY1 caenorhabdi
14	29	93.5	903	2 Q9VUM8	Q9VUM8 drosophila
15	29	93.5	971	2 Q7KUM3	Q7KUM3 drosophila
16	29	93.5	971	2 AAS65000	AAS65000 drosophila
17	28	90.3	153	2 Q92DM3	Q92DM3 listeria in
18	28	90.3	153	2 Q8Y8U5	Q8Y8U5 listeria mo
19	28	90.3	153	2 Q722C0	Q722C0 listeria mo
20	28	90.3	153	2 AAT03594	AAT03594 listeria
21	28	90.3	296	2 Q72R88	Q72R88 leptospira
22	28	90.3	296	2 Q8F417	Q8F417 leptospira
23	28	90.3	296	2 AAS70446	AAS70446 leptospira
24	28	90.3	308	2 Q8GDE4	Q8GDE4 heterodera
25	28	90.3	309	2 Q6MH57	Q6MH57 bdellovibri
26	28	90.3	309	2 CAE81070	CAE81070 bdellovibri
27	28	90.3	316	2 Q90428	Q90428 brachydanio
28	28	90.3	569	2 Q88F13	Q88F13 pseudomonas
29	28	90.3	633	1 DNAK AGRT5	P50019 agrobacteri
30	28	90.3	634	2 Q6RSN6	Q6RSN6 agrobacteri
31	28	90.3	634	2 AAR84665	AAR84665 agrobacteri

32	28	90.3	638	1 DNAK RHILE	O33528 rhizobium 1
33	28	90.3	638	1 DNAK RHILE	Q986d1 rhizobium 1
34	28	90.3	686	2 Q9KF22	Q9KF22 bacillus ha
35	28	90.3	845	2 Q9PFF4	Q9PFF4 xyella fas
36	28	90.3	969	2 BAC86701	BAC86701 homo sapi
37	28	90.3	1424	2 Q75DK8	Q75DK8 ashbya goss
38	28	90.3	1424	2 AAS50783	AAS50783 ashbya go
39	28	90.3	1522	1 ARHB HUMAN	O15085 homo sapien
40	28	90.3	1562	2 Q6PFW2	Q6PFW2 homo sapien
41	28	90.3	1562	2 AAH57394	AAH57394 homo sapi
42	28	90.3	2691	2 CAG26692	CAG26692 mus muscu
43	28	90.3	2697	2 CAG26691	CAG26691 mus muscu
44	28	90.3	2798	1 NPBL MOUSE	Q6KCD5 mus musculu
45	28	90.3	2798	2 CAF25291	CAF25291 mus muscu

ALIGNMENTS

RESULT 1

ID	YGIM HAEIN	STANDARD	PRT	203 AA
AC	P44272			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Hypothetical protein HI1605 precursor.			
GN	OrderedLocNames=HI1605;			
OS	Haemophilus influenzae.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;			
OC	Pasteurellaceae; Haemophilus.			
OX	NCBI_TaxID=727;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Rd / KW20 / ATCC 51907;			
RA	MEDLINE=95350630; PubMed=7542800;			
RA	Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,			
RA	Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,			
RA	McKenney K., Sutton G.G., FitzHugh W., Fields C.A., Gocayne J.D.,			
RA	Scott J.B., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,			
RA	Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,			
RA	Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,			
RA	Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,			
RA	Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,			
RT	Venter J.C.;			
RT	"Whole-Genome random sequencing and assembly of Haemophilus influenzae			
RL	Rd.";			
RL	Science 269:496-512(1995).			
CC	-1- SIMILARITY: Strong, to E.coli ygiM.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	-----			
DR	EMBL; U32834; AAC23249.1; -			
DR	PIR; C64038; C64038.			
DR	TIGR; HI1605;			
DR	InterPro; IPR003646; SH3_bac.			
DR	SMART; SM00287; SH3b; 1.			
DR	Complete proteome; Hypothetical protein; Signal; Transmembrane.			
FT	SIGNAL 1 23 Potential..			
FT	CHAIN 24 203 Hypothetical protein HI1605.			
FT	TRANSMEM 157 189 Potential.			
SQ	SEQUENCE 203 AA; 23112 MW; FAFCSER29FD29C05 CRC64;			

Query Match

Best Local Similarity 100.0%; Score 31; DB 1; Length 203;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKISR 7
Db 103 LTLKISR 103

RESULT 2
Q986H5 Q986H5 PRELIMINARY; PRT; 367 AA.
AC Q986H5
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Muconate lactonizing enzyme.
GN OrderedLocusNames=ml17353;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=391;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=MAFF303099;
RC MEDLINE=21082936; PubMed=11214974;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti (supplement).";
RL DNA Res. 7:381-406(2000).
DR EMBL; AF03011; BAB53478.1; --
DR HSP; G34508; IJFW.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001354; MR_MLE.
DR Pfam; PF01188; MR_MLE; 1.
DR Pfam; PF02746; MR_MLE_N; 1.
KW Complete proteome.
SQ SEQUENCE 367 AA; 39526 MW; 5E76121793FAD48A CRC64;

Query Match 93.5%; Score 29; DB 2; Length 367;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKISR 7
Db 262 LTLKISR 268

RESULT 3
Q6NI26 Q6NI26 PRELIMINARY; PRT; 459 AA.
AC Q6NI26;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ABC transport system ATP-binding protein.
GN OrderedLocusNames=DIP0953;
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacterium.

OX NCBI_TaxID=1717;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Biotype gravis / NCTC 13129;
RC MEDLINE=22965443; PubMed=14602910;
RA Cerdano-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zeyza A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RA "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129.";
RL Nucleic Acids Res. 31:6516-6523(2003).
[1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; BX248356; CAE49472.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_TRANSPORTER.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_TRANSPORTER; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 459 AA; 49537 MW; 373303B91C33A816 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 459;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKISR 7
Db 25 LTLKISR 31

RESULT 4
CAE49472 CAE49472 PRELIMINARY; PRT; 459 AA.
AC CAE49472;
DT 02-WAR-2004 (TrEMBLrel. 27, Created)
DT 02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ABC transport system ATP-binding protein.
GN DIP0953.
OS Corynebacterium diphtheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=Biotype gravis / NCTC 13129;
RC MEDLINE=22965443; PubMed=14602910;
RA Cerdano-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
RA Pallen M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zeyza A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinowitsch E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RA "The complete genome sequence and analysis of Corynebacterium
RT diphtheriae NCTC13129.";
RL Nucleic Acids Res. 31:6516-6523(2003).
DR EMBL; BX248356; CAE49472.1; --
KW ATP-binding.
SQ SEQUENCE 459 AA; 49537 MW; 373303B91C33A816 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 459;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKISR 7
Db 25 LTLKISR 31

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Hwang B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y.,
RA Walker M.A., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B.,
RA Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I.,
RA Lenz C.C., Li J.J., Liu S.S., Luros G.S., Rowley D.D., Schwartz J.J.,
RA Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W.,
RA Federspiel N.N.A., Theologis A.A., Ecker J.J.R.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
DR EMBL: AC0023328; AAF79436.1; -.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR008566; FBD.
DR InterPro: IPR008945; Skp1_skp2.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00579; FBD; 1.
DR SMART: SM00256; FBOX; 1.
DR PROSITE: PS50181; FBOX; 1.
SQ SEQUENCE 326 AA; 60437 MW; 6C45C35BED85B749 CRC64;
Query Match 93.5%; Score 29; DB 2; Length 526;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTKLSR 7
DB 294 LTKLSR 300
|||||
RESULT 7
O23360 PRELIMINARY; PRT; 555 AA.
ID O23360
AC O23360;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein AT4G15060.
GN Name=AT4G15060; Synonyms=AT4G15060;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9812113; PubMed=9461215;
RA Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Bergkamp R., Dirke W., van Staveren M., Stiekema W., Drost L.,
RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffanelli P., Wedler H.

Wedler E., Wambutt R., Weitzneger T., Pohl T.M., Terryn N.,
Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,
Entian K.D., Rieger M., Schaeffer M., Funk B., Mueller-Auer S.,
Sivilev M., James R., Montfort A., Pons A., Puigdomenech P., Douka A.,
Vouklatou E., Milioni D., Hatzipoulos P., Piravandi E., Obermaier B.,
Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
Delseny M., Voet M., Volckaert G., Mewes H.W., Klosterman S.,
Schueller C., Chalwatzis N.;
RT Arabidopsis thaliana";
RL Nature 391:485-488(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97337; CAB10285.1; -.
DR EMBL; AL161540; CAB578548.1; -.
DR FIR; C71414; C71414; F-box.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR006566; FBD.
DR InterPro; IPR008945; Skp1_Skp2.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00579; FBD; 1.
KW Hypothetical protein.
KW SEQUENCE 555 AA; 93199 MW; C8D02D8C05481FFB CRC64;
Query Match 93.5%; Score 29; DB 2; Length 555;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTKLSR 7
DB 411 LTKLSR 417
ID Q74H59 PRELIMINARY; PRT; 636 AA.
AC Q74H59;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chapterone protein dnak.
GN Name=dnak; ORFNames=GSU0033;
OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Meche B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Gwinn T.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidtsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
environments";
RL Science 302:1967-1969(2003).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AE047180; AAR33368.1; -.
DR TIGR; GSU0033; -.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70; 1; 1.
DR PROSITE; PS00329; HSP70; 2; 1.
DR

RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF125964; AAL13765.1; -.
DR HSP; P31751; IGZK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF02149; KAL; 1.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00118; PROTEIN_KINASE_ST; UNKNOWN_1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Hypothetical protein; Kinase; Transferase.
SQ SEQUENCE 722 AA; 82249 MW; C3C3E2AB5CEB6FB8 CRC64;

Query Match 93.5%; Score 29; DB 2; Length 722;
Best Local Similarity 85.7%; Pred.No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 512 LTLKLSR 518

RESULT 13
Q9UAY1 PRELIMINARY; PRT; 726 AA.
AC Q9UAY1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein W03G1.6.
GN ORFNames=W03G1.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF125964; AAD14754.1; -.
DR HSP; Q63450; LA06.
DR WormPep; W03G1.6; CB17284.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

Q9UAY1 PRELIMINARY; PRT; 903 AA.
AC Q9UAY1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG7255-PB (CG7255-pa).
GN ORFNames=CG7255;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gortell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RA FLYBASE;
 RL [6]
 RP SEQUENCE FROM N.A.
 RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RA EMBL; AE003531; AAF49646.2; -;
 RA FLYBASE; FBGN0036493; CG7255.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0006865; P:amino acid transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002293; AA/re1_permease1.
 DR InterPro; IPR004841; Permease region.
 DR Pfam; PF00324; AA_permease; 1.
 KW Transmembrane; Transport.
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 Query Match 93.5%; Score 29; DB 2; Length 903;
 Best Local Similarity 85.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LTKLSR 7
 Db 596 ITKLSR 602
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 ID Q7KUM3 PRELIMINARY; PRT; 971 AA.

AC Q7KUM3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG7255-PD (CG7255-pe).
 GN ORFNames=CG7255;
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophila;
 OX Ephydroidea; Drosophilidae; Drosophila.
 OX [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Besu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Ciesla M., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Foele C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheier F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodagef, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

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RN  [4]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22426069; PubMed=12537572;
RA  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA  Hradecky P., Huang Y., Kanink J.S., Millburn G.H., Prochnik S.E.,
RA  Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA  Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA  Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA  Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA  Lewis S.E.;
RT  "Annotation of the Drosophila melanogaster euchromatic genome: a
RT  systematic review.";
RL  Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN  [5]
RP  SEQUENCE FROM N.A.
RG  FLYBASE;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN  [6]
RP  SEQUENCE FROM N.A.
RG  FLYBASE;
RL  Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL: AE003531; AAS65000.1; -.
DR  InterPro: IPR002293; AA/rel_permeasel.
DR  InterPro: IPR004841; Permease_region.
DR  Pfam: PF00324; AA_permease; 1.
KW  Transmembrane; Transport.
SQ  SEQUENCE 971 AA; 106747 MW; 919608FD06398DF0 CRC64;

Query Match          93.5%; Score 29; DB 2; Length 971;
Best Local Similarity 85.7%; Pred.No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 ITIKLSR 7
DB  664 ITIKLSR 670

Search completed: November 4, 2004, 00:53:59
Job time : 105 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 seconds
(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-13

Perfect score: 31

Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	29	93.5	113	2 AAW13517	Aaw13517 Anti-mela
2	29	93.5	131	2 AAR20065	Aar20065 MRK16-L c
3	29	93.5	638	8 ADJ49770	Adj49770 Oil-assoc
4	29	93.5	641	8 ADJ49389	Adj49389 Oil-assoc
5	29	93.5	641	8 ADJ50245	Adj50245 Oil-assoc
6	29	93.5	870	4 ABB66159	Abb66159 Drosophil
7	29	93.5	880	4 ABB63131	Abb63131 Drosophil
8	28	90.3	153	5 ABB49428	Abb49428 Listeria
9	28	90.3	155	4 AAG72986	Aag72986 Oilfactory
10	28	90.3	212	4 AAB90806	Aab90806 Human she
11	28	90.3	374	3 AAB42328	Aab42328 Human ORF
12	28	90.3	474	3 AAY56509	Aay56509 Human Jur
13	28	90.3	633	8 ADJ49412	Adj49412 Oil-assoc
14	28	90.3	638	8 ADJ49826	Adj49826 Oil-assoc
15	28	90.3	638	8 ADJ49161	Adj49161 Oil-assoc
16	28	90.3	1520	2 AAY41010	Aay41010 Amino aci
17	28	90.3	1522	8 ADF45494	Adf45494 Human KIA
18	28	90.3	1522	8 ADH23366	Adh23366 Human gua
19	28	90.3	1562	8 ADQ17442	Adq17442 Human sof
20	28	90.3	1562	8 ADF45522	Adf45522 Human KIA
21	28	90.3	1562	8 ADF45496	Adf45496 Human KIA
22	28	90.3	1736	7 ADE08492	Ade08492 Novel pro
23	28	90.3	2685	7 ADC06796	Adc06796 Human pro
24	28	90.3	2804	8 ADN04576	Adn04576 Antipsori
25	27	87.1	31	6 ABO04917	Ab004917 Human col

26	27	87.1	127	2 AAW1254	Aaw1254 Murine an
27	27	87.1	127	2 AAW76124	Aaw76124 Murine IC
28	27	87.1	127	2 AAW81448	Aaw81448 Murine an
29	27	87.1	127	2 AAY00781	Aay00781 Antibody
30	27	87.1	127	3 AAY50751	Aay50751 Murine an
31	27	87.1	127	3 AAB13044	Aab13044 Murine IC
32	27	87.1	127	3 AAY82443	Aay82443 Murine an
33	27	87.1	127	5 AAU70936	Aau70936 Murine mo
34	27	87.1	127	7 ADG25695	Adg25695 Mouse ant
35	27	87.1	133	3 AAY93726	Aay93726 The kappa
36	27	87.1	133	6 AAE35910	Aae35910 Human 12.
37	27	87.1	139	6 ABM73321	Abm73321 Staphyloc
38	27	87.1	141	5 ABP38865	Abp38865 Staphyloc
39	27	87.1	189	4 AAU36206	Aau36206 Pseudomon
40	27	87.1	189	6 ABU38277	Abu38277 Protein e
41	27	87.1	191	6 ABU35748	Abu35748 Protein e
42	27	87.1	193	4 AAU52716	Aau52716 Propionib
43	27	87.1	193	6 ABM49235	Abm49235 Propionib
44	27	87.1	221	7 ABO68708	Ab068708 Pseudomon
45	27	87.1	239	3 AAY82611	Aay82611 Human PTH

ALIGNMENTS

RESULT 1
AAW13517
ID AAW13517 standard; protein; 113 AA.
XX AC AAW13517;
XX
DT 28-OCT-1997 (first entry)
XX
DE Anti-melanoma light chain antibody clone D33.
XX
KW Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
KW cancer; tumorigenesis; anticancer vaccine.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 24..39
FT /label= CDR1
FT Misc-difference 47
FT /label= His, Gly
FT Region 55..61
FT /label= CDR2
FT Region 94..102
FT Misc-difference 95
FT /label= CDR3
FT /label= His, Gln
WO9702479-A2.
23-JAN-1997.
28-JUN-1996; 96WO-IE001032.
30-JUN-1995; 95US-00497647.
(UYVA) UNIV YALE.
Garen A, Cai X;
WPI; 1997-109061/10.
Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion
phage library produced using peripheral blood lymphocytes from a cancer
patient.
Claim 19; Page 55; 82pp; English.
A process for isolating and synthesising human monoclonal anti-tumour

antibodies has been produced. The process involves: (a) constructing at least one fusion phage library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phage library in a binding assay with cultured tumour cells of the same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phage selected in step (b) and (c); (e) assaying the specificity of the cloned phage by incubating the phage with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phage that do not bind to either cell line of cultured normal cells in further binding assays to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human light chain antibody, from an scrv antibody fusion phage library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour antigens for studying tumourigenesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MAbs). Since the antibodies are isolated from fusion phage libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations

Sequence 113 AA;

Query Match 93.5%; Score 29; DB 2; Length 113;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
| | | | |
Db 76 LTLKISR 82

RESULT 2
AAR20065
ID AAR20065 standard; protein; 131 AA.
XX
AC AAR20065;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1992 (first entry)
XX
XX MRK16-L chain.
DE
XX Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
KW Homo; sapiens.
XX Mus musculus.
OS Chimeric.
XX JP03254691-A.
FN 13-NOV-1991.
PD
XX 02-MAR-1990; 90JP-00051563.
PF
XX 02-MAR-1990; 90JP-00051563.
PR
XX (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX
XX WPI; 1992-002461/01.
DR N-PSDB; AAQ20071.
XX
XX Chimeric antibody against drug resistant cancer - comprises variable region homologous to region in mouse monoclonal antibody and constant region homologous to region in human immunoglobulin.
PT
XX Disclosure; Fig 5; 20pp; Japanese.
PS
XX A chimeric antibody against drug-resistant cancer consists of (1) a variable region having an amino acid sequence homologous to a variable

region in the mouse monoclonal antibody against drug- resistance and (2) a constant region having an amino acid sequence homologous to the constant region in human immunoglobulin. The chimeric antibody selectively inhibits the growth of cancer cells showing drug resistance or enhances the sensitivity to the drug. The antibody is very low in immunogenicity. The MK16-H chain is shown in AAQ20070. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)

Sequence 131 AA;

Query Match 93.5%; Score 29; DB 2; Length 131;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKISR 7
| | | | |
Db 95 LTLKISR 101

RESULT 3
ADJ49770
ID ADJ49770 standard; protein; 638 AA.
XX
AC ADJ49770;
XX
DT 06-MAY-2004 (first entry)
XX
XX Oil-associated gene related protein #1270.
DE
XX oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
KW Unidentified.
XX US2004025202-A1.
FN
XX 05-FEB-2004.
PD
XX 14-MAR-2003; 2003US-00389556.
PF
XX 15-MAR-2002; 2002US-0365301P.
PR 26-JUN-2002; 2002US-0391786P.
PR 26-JUN-2002; 2002US-0392018P.
XX
XX (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX WPI; 2004-142683/14.
DR
XX Novel recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene for producing transgenic plant seed.
PT
XX Example 3; SEQ ID NO 1774; 22pp; English.
PS
XX The invention relates to a recombinant DNA construct comprising a promoter functional in plants operably linked to an oil-associated gene. The construct is useful for transgenic plant seed which has in its genome the construct, that is functional in the plant to transcribe the oil-associated gene. The transgenic plant seed grows into a plant having enhanced seed oil as compared to wild type. The construct is useful for producing hybrid maize seed. The transgenic plant seed is useful for producing vegetable oil. The present sequence represents the amino acid sequence of an oil-associated gene related protein.
XX
XX Sequence 638 AA;

Query Match 93.5%; Score 29; DB 8; Length 638;


```

XX PD 27-SEP-2001.
XX PF
XX PR 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEXE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL10262.
XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 25269; 21pp + Sequence Listing; English.
XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 870 AA;
XX
XX Query Match 93.5%; Score 29; DB 4; Length 870;
XX Best Local Similarity 85.7%; Pred. NO. 9.6e+02;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LTLKLSR 7
XX DB 563 ITLKLSR 569
XX
XX RESULT 7
XX ABB63131
XX ID ABB63131 standard; protein; 880 AA.
XX AC ABB63131;
XX
XX DT 26-MAR-2002 (first entry)
XX
XX DE Drosophila melanogaster polypeptide SEQ ID NO 16185.
XX
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX
XX OS Drosophila melanogaster.
XX
XX PN WO200171042-A2.
XX
XX PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2001WO-US009231.
XX
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX
XX PA (PEXE ) PE CORP NY.
XX
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL07234.
XX

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XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 16185; 21pp + Sequence Listing; English.
XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX CC ABB72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 880 AA;
XX
XX Query Match 93.5%; Score 29; DB 4; Length 880;
XX Best Local Similarity 85.7%; Pred. NO. 9.7e+02;
XX Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 LTLKLSR 7
XX DB 573 ITLKLSR 579
XX
XX RESULT 8
XX ABB49428
XX ID ABB49428 standard; protein; 153 AA.
XX AC ABB49428;
XX
XX DT 05-FEB-2002 (first entry)
XX
XX DE Listeria monocytogenes protein #2132.
XX
XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
XX KW vitamin B12; bacterial infection; disease.
XX
XX OS Listeria monocytogenes.
XX
XX PN WO200177335-A2.
XX
XX PD 18-OCT-2001.
XX
XX PF 11-APR-2001; 2001WO-FR001118.
XX
XX PR 11-APR-2000; 2000FR-00004629.
XX
XX PA (INSP ) INST PASTEUR.
XX
XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
XX PI Dussurget O, Chetoui F, Medjari H, Glaser P, Kunst F, Cossart P;
XX PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
XX PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
XX PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
XX PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
XX PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
XX PI Rose M, Voss H;
XX
XX DR WPI; 2002-010914/01.
XX
XX PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX PT and prevention of Listeria and related bacterial infections, and related
XX PT polypeptides.
XX
XX PS Claim 6; SEQ ID NO 2133; 192pp; French.
XX
XX CC The present invention relates to the genome sequence of Listeria
XX CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of

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CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of L. monocytes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccine compositions for the treatment or prevention of infections by L.
 CC monocytes and related organisms. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 153 AA;

Query Match 90.3%; Score 28; DB 5; Length 153;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKLSR 7
 DB 98 LTKLSK 104

RESULT 9
 AAG72986
 ID AAG72986 standard; protein; 155 AA.
 XX
 AC AAG72986;
 DT 30-JUL-2001 (first entry)
 XX
 DE Olfactory receptor-like polypeptide, SEQ ID NO: 2668.
 KW Human; olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX
 OS Unidentified.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000; 2000WO-US027582.
 XX
 PR 08-OCT-1999; 99US-0158615P.
 XX
 PR 24-FEB-2000; 2000US-0184803P.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI; 2001-290713/30.
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists.
 XX
 PS Example 6; Page 1804; 1857pp; English.

CC The present sequence is an olfactory receptor polypeptide which was used
 CC as a query sequence in a database search of olfactory receptor (OR)-like
 CC sequences. The invention relates to isolated polynucleotides encoding
 CC polypeptides involved in olfactory sensation. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification of
 CC the odour receptors used to detect these primary scents. The methods also
 CC enable determination of secondary scents and the identification of

CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals
 XX
 SQ Sequence 155 AA;

Query Match 90.3%; Score 28; DB 4; Length 155;
 Best Local Similarity 85.7%; Pred. No. 2.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKLSR 7
 DB 35 LTKLSR 41

RESULT 10
 AAB90806
 ID AAB90806 standard; protein; 212 AA.
 XX
 AC AAB90806;
 DT 15-JUN-2001 (first entry)
 XX
 DE Human shear stress-response protein SEQ ID NO: 112.
 KW Human; shear stress-response protein; vascular disease; arteriosclerosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200125427-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 02-OCT-2000; 2000WO-JP006840.
 XX
 PR 01-OCT-1999; 99JP-00280976.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 PA (NOJI/) NOJIMA H.
 XX
 PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
 PI Kuga T, Sekine S, Nakamura Y, Sugano S;
 XX
 DR WPI; 2001-266308/27.
 DR N-PSDB; AAH02929.
 XX
 PT DNA sequences, proteins encoded by them and antibodies against them
 PT useful in diagnosis and treatment of vascular disease caused by
 PT arteriosclerosis.
 XX
 PS Claim 52; Page 551-552; 678pp; Japanese.

CC The present invention provides the protein and coding sequences of a
 CC number of human shear stress response proteins. These are useful in the
 CC diagnosis, treatment and screening of vascular diseases caused by
 CC arteriosclerosis, including heart failure, post-PTCA restenosis and
 CC hypertension
 XX
 SQ Sequence 212 AA;

Query Match 90.3%; Score 28; DB 4; Length 212;
 Best Local Similarity 85.7%; Pred. No. 3.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKLSR 7
 DB 200 LTKLSK 206

RESULT 11

AAB42328
ID AAB42328 standard; protein; 374 AA.
XX
AC AAB42328;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2092 polypeptide sequence SEQ ID NO:4184.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
FN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
FA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC76537.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 3376-3377; 5507pp; English.
XX
AA AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
CC antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antirheumatic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 374 AA;

Query Match 90.3%; Score 28; DB 3; Length 374;
Best Local Similarity 85.7%; Pred. No. 6.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTKLSR 7
DB 226 LTKLSR 232
RESULT 12
AAAY56509
ID AAY56509 standard; protein; 474 AA.
XX
AC AAY56509;
XX
DT 17-FEB-2000 (first entry)
XX
DE Human Jurkat cell clone 2-9 AIM2 complementary strand ORF protein.
XX
KW Human; Jurkat cell; tumour necrosis factor receptor releasing enzyme;
KW TRRR; cytokine; TNF; identification; cytostatic; anti-inflammatory;
KW cardiant; immunomodulator; antirheumatic; antibacterial; cancer;
KW heart failure; cachexia; inflammation; endotoxin shock; arthritis;
KW multiple sclerosis; sepsis.
XX
OS Homo sapiens.
XX
FN WO9958559-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99WO-US010793.
XX
PR 14-MAY-1998; 98US-00081385.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Gatanaga T, Granger GA;
XX
DR WPI; 2000-039067/03.
DR N-PSDB; AAZ38863.
XX
PT Tumour necrosis factor receptor releasing enzyme modulators and
PT polynucleotides.
XX
PS Example 5; Page 96-97; 106pp; English.
XX
AA The present invention describes isolated polynucleotides (A) comprising a
CC sequence expressed at the mRNA level in Jurkat T cells and showing
CC increased enzymatic activity for cleaving and releasing the tumour
CC necrosis factor (TNF) receptor in genetically modified COS-1 cells
CC expressing the receptor. Methods from the present invention can be used
CC to assess a disease condition associated with altered TRRE activity. The
CC polypeptides, polynucleotides and antibodies can be used to decrease or
CC increase signal transduction from a cytokine in a cell. The polypeptides,
CC polynucleotides and antibodies may be used to treat heart failure,
CC cachexia, inflammation, endotoxin shock, arthritis, multiple sclerosis
CC and sepsis, and cancer. The present sequence represents the longest open
CC reading frame encoded by the complementary strand of the AIM2 clone which
CC affects tumour necrosis factor receptor releasing enzyme (TRRE) activity
XX
SQ Sequence 474 AA;
Query Match 90.3%; Score 28; DB 3; Length 474;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTKLSR 7
DB 358 LTKLSR 364

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RESULT 13
ADJ49412
ID ADJ49412 standard; protein; 633 AA.
XX
AC ADJ49412;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #912.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
FN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
PS Example 3; SEQ ID NO 1416; 22pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 633 AA;
XX
Query Match 90.3%; Score 28; DB 8; Length 633;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
| | | | |
DB 291 LTLKLTR 297

RESULT 14
ADJ49826
ID ADJ49826 standard; protein; 638 AA.
XX
AC ADJ49826;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #1326.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
FN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
XX
DR WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT plant seed.
XX
PS Example 3; SEQ ID NO 1416; 22pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 633 AA;
XX
Query Match 90.3%; Score 28; DB 8; Length 633;
Best Local Similarity 85.7%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
| | | | |
DB 291 LTLKLTR 297

RESULT 15
ADJ49161
ID ADJ49161 standard; protein; 638 AA.
XX
AC ADJ49161;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #661.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
FN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX

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OS Unidentified.
XX
XX US2004025202-A1.
XX
XX 05-FEB-2004.
XX
XX 14-MAR-2003; 2003US-00389566.
XX
XX 15-MAR-2002; 2002US-0365301P.
XX
XX 26-JUN-2002; 2002US-0391786P.
XX
XX 26-JUN-2002; 2002US-0392018P.
XX
XX (LAUR/) LAURIE C C.
XX
XX (RAVA/) RAVANELLO M.
XX
XX (SAVA/) SAVAGE T.
XX
XX (LEDE/) LEDEUX J R.
XX
XX (ROGE/) ROGERS J A.
XX
XX Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
XX
XX WPI; 2004-142683/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX
XX Example 3; SEQ ID NO 1830; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents the amino acid
XX sequence of an oil-associated gene related protein.
XX
XX Sequence 638 AA;
XX
Query Match 90.3%; Score 28; DB 8; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
| | | | |
DB 291 LTLKLTR 297

RESULT 15
ADJ49161
ID ADJ49161 standard; protein; 638 AA.
XX
AC ADJ49161;
XX
DT 06-MAY-2004 (first entry)
XX
DE Oil-associated gene related protein #661.
XX
KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
XX
OS Unidentified.
XX
FN US2004025202-A1.
XX
PD 05-FEB-2004.
XX
PF 14-MAR-2003; 2003US-00389566.
XX
PR 15-MAR-2002; 2002US-0365301P.
XX
PR 26-JUN-2002; 2002US-0391786P.
XX
PR 26-JUN-2002; 2002US-0392018P.
XX

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PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
XX
PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX
XX WPI; 2004-142683/14.
XX
PT Novel recombinant DNA construct comprising a promoter functional in
PT plants operably linked to an oil-associated gene for producing transgenic
PT Plant seed.
XX
PS Example 3; SEQ ID NO 1165; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in plants operably linked to an oil-associated gene.
CC The construct is useful for transgenic plant seed which has in its genome
CC the construct, that is functional in the plant to transcribe the oil-
CC associated gene. The transgenic plant seed grows into a plant having
CC enhanced seed oil as compared to wild type. The construct is useful for
CC producing hybrid maize seed. The transgenic plant seed is useful for
CC producing vegetable oil. The present sequence represents the amino acid
CC sequence of an oil-associated gene related protein.
XX
SQ Sequence 638 AA;
Query Match 90.3%; Score 28; DB 8; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LTLKLSR 7
Db 291 LTLKLTR 297
Search completed: November 4, 2004, 00:47:44
Job time : 63.3333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 Seconds
(without alignments)
31.376 Million cell updates/sec

Title: US-09-712-819D-13
Perfect score: 31
Sequence: 1 LTKLSR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215900 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	382	14	US-10-369-493-5663
2	29	93.5	638	15	US-10-389-566-1774
3	29	93.5	641	15	US-10-389-566-1393
4	29	93.5	641	15	US-10-389-566-2249
5	29	93.5	726	14	US-10-369-493-5945
6	28	90.3	474	9	US-09-752-639-148
7	28	90.3	474	9	US-09-984-198-148
8	28	90.3	629	14	US-10-369-493-11797
9	28	90.3	630	14	US-10-369-493-14521
10	28	90.3	633	14	US-10-369-493-14213
11	28	90.3	633	14	US-10-369-493-14987
12	28	90.3	633	15	US-10-389-566-1416
13	28	90.3	638	14	US-10-369-493-12088

14	28	90.3	638	15	US-10-389-566-1165	Sequence 1165, Ap
15	28	90.3	638	15	US-10-389-566-1830	Sequence 1830, Ap
16	28	90.3	1522	14	US-10-134-102-8	Sequence 8, Appl
17	28	90.3	1522	14	US-10-144-198-31	Sequence 31, Appl
18	28	90.3	2697	14	US-10-144-198-12	Sequence 12, Appl
19	27	87.1	31	14	US-10-001-883-131	Sequence 131, App
20	27	87.1	66	15	US-10-424-599-190772	Sequence 190772, App
21	27	87.1	123	15	US-10-424-599-281882	Sequence 281882, App
22	27	87.1	127	9	US-09-753-436-45	Sequence 45, Appl
23	27	87.1	127	14	US-10-163-942-45	Sequence 45, Appl
24	27	87.1	132	15	US-10-424-599-161373	Sequence 161373, App
25	27	87.1	133	14	US-10-153-382-39	Sequence 39, Appl
26	27	87.1	189	9	US-09-813-242-11799	Sequence 11799, A
27	27	87.1	189	15	US-10-282-122A-66201	Sequence 66201, A
28	27	87.1	189	15	US-10-424-599-158936	Sequence 158936, A
29	27	87.1	191	15	US-10-282-122A-63672	Sequence 63672, A
30	27	87.1	259	15	US-10-289-762-366	Sequence 366, App
31	27	87.1	259	15	US-10-282-122A-54805	Sequence 54805, A
32	27	87.1	259	15	US-10-282-122A-55147	Sequence 55147, A
33	27	87.1	291	15	US-10-424-599-209007	Sequence 209007, App
34	27	87.1	626	15	US-10-380-533-144	Sequence 144, App
35	27	87.1	645	15	US-10-389-566-1037	Sequence 1037, App
36	27	87.1	706	15	US-10-380-533-134	Sequence 134, App
37	27	87.1	707	15	US-10-380-533-142	Sequence 142, App
38	26	83.9	35	15	US-10-424-599-163720	Sequence 163720, App
39	26	83.9	42	15	US-10-424-599-159705	Sequence 159705, App
40	26	83.9	57	15	US-10-424-599-277603	Sequence 277603, App
41	26	83.9	60	9	US-09-864-761-43672	Sequence 43672, A
42	26	83.9	66	9	US-09-867-550-1190	Sequence 1190, Ap
43	26	83.9	74	15	US-10-424-599-176978	Sequence 176978, App
44	26	83.9	77	15	US-10-424-599-279709	Sequence 279709, App
45	26	83.9	78	15	US-10-424-599-191620	Sequence 191620, App

ALIGNMENTS

RESULT 1

US-10-369-493-5663
; Sequence 5663, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 39-10(52052)B
; CURRENT APPLICATION NUMBER: US/10369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5663
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5663

Query Match 100.0%; Score 31; DB 14; Length 382;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTKLSR 7

DB 73 LTKLSR 79

RESULT 2

US-10-389-566-1774
; Sequence 1774, Application US/10389566

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; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1774
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Geobacter metallireducens
US-10-389-566-1774

Query Match          93.5%; Score 29; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTKLSR 297

RESULT 3
US-10-389-566-1393
; Sequence 1393, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1393
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-389-566-1393

Query Match          93.5%; Score 29; DB 15; Length 641;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTKLSR 297

RESULT 4
US-10-389-566-2249
; Sequence 2249, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
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; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2249
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-389-566-2249

Query Match          93.5%; Score 29; DB 15; Length 641;
Best Local Similarity 85.7%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTKLSR 297

RESULT 5
US-10-369-493-5945
; Sequence 5945, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5945
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5945

Query Match          93.5%; Score 29; DB 14; Length 726;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 512 LTKLSR 518

RESULT 6
US-09-752-639-148
; Sequence 148, Application US/09752639
; Patent No. US20020091243A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
```

```

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/752,639
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-752-639-148

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Query Match 90.3%; Score 28; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 358 LTLRLSR 364

RESULT 7
US-09-984-198-148
; Sequence 148, Application US/09984198
; Patent No. US20020106679A1
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/984,198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE:
; APPLICATION NUMBER: 09/081,385
; FILING DATE:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-984-198-148

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Query Match 90.3%; Score 28; DB 9; Length 474;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 358 LTLRLSR 364

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RESULT 8
US-10-369-493-11797
; Sequence 11797, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11797
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11797

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Query Match 90.3%; Score 28; DB 14; Length 629;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
Db 291 LTLKLSR 297

RESULT 9

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US-10-369-493-14521
; Sequence 14521, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14521
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14521

Query Match          90.3%; Score 28; DB 14; Length 630;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLSR 297

RESULT 10
US-10-369-493-14213
; Sequence 14213, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14213
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14213

Query Match          90.3%; Score 28; DB 14; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLSR 297

RESULT 11
US-10-369-493-14987
; Sequence 14987, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14987
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14987

Query Match          90.3%; Score 28; DB 14; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLSR 297

RESULT 12
US-10-389-566-1416
; Sequence 1416, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1416
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-389-566-1416

Query Match          90.3%; Score 28; DB 15; Length 633;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LTLKLSR 7
Db 291 LTLKLSR 297

RESULT 13
US-10-369-493-12088
; Sequence 12088, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
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; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12088
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-369-493-12088

Query Match 90.3%; Score 28; DB 14; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
|||:|
Db 291 LTLKLTR 297

RESULT 14

US-10-389-566-1165
; Sequence 1165, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1165
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-389-566-1165

Query Match 90.3%; Score 28; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
|||:|
Db 291 LTLKLTR 297

RESULT 15

US-10-389-566-1830
; Sequence 1830, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1830

; LENGTH: 638
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-10-389-566-1830

Query Match 90.3%; Score 28; DB 15; Length 638;
Best Local Similarity 85.7%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LTLKLSR 7
|||:|
Db 291 LTLKLTR 297

Search completed: November 4, 2004, 01:13:30
Job time : 73.3333 secs

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	72.7	7	1	US-08-222-619-8
2	24	72.7	7	5	PCT-US95-04075-8
3	20	60.6	7	4	US-09-423-468A-6
4	19	57.6	6	1	US-08-222-619-21
5	19	57.6	6	5	PCT-US95-04075-21
6	19	57.6	7	1	US-08-136-743B-55
7	19	57.6	7	3	US-08-040-216-28
8	18	54.5	6	1	US-08-297-731-4
9	18	54.5	6	3	US-09-623-618B-6
10	18	54.5	6	4	US-09-657-332A-6
11	18	54.5	6	4	US-09-876-388-6
12	18	54.5	6	5	PCT-US95-10793-4
13	18	54.5	7	1	US-08-237-731-5
14	18	54.5	7	3	US-09-623-618B-7
15	18	54.5	7	3	US-09-218-363-23
16	18	54.5	7	4	US-09-657-332A-7
17	18	54.5	7	4	US-09-876-388-7
18	18	54.5	7	4	US-08-753-750B-20
19	18	54.5	7	5	PCT-US95-10793-5
20	17	51.5	5	1	US-08-136-743B-63
21	17	51.5	5	3	US-09-040-216-55
22	17	51.5	5	3	US-08-591-632-23
23	17	51.5	5	3	US-09-611-451-23
24	17	51.5	6	1	US-08-136-743B-62
25	17	51.5	6	3	US-09-040-216-54
26	17	51.5	6	3	US-09-187-859-636
27	17	51.5	6	3	US-09-187-859-650

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28 17 51.5 6 4 US-09-522-433B-12 Sequence 12, Appl
29 17 51.5 6 4 US-09-839-542B-636 Sequence 636, App
30 17 51.5 6 4 US-09-839-542B-650 Sequence 650, App
31 17 51.5 7 1 US-09-393-941-2 Sequence 2, Appli
32 17 51.5 7 1 US-08-136-743B-6 Sequence 6, Appli
33 17 51.5 7 1 US-08-136-743B-29 Sequence 29, Appl
34 17 51.5 7 1 US-08-136-743B-33 Sequence 33, Appl
35 17 51.5 7 1 US-08-136-743B-37 Sequence 37, Appl
36 17 51.5 7 1 US-08-136-743B-54 Sequence 54, Appl
37 17 51.5 7 1 US-08-136-743B-56 Sequence 56, Appl
38 17 51.5 7 1 US-08-136-743B-57 Sequence 57, Appl
39 17 51.5 7 1 US-08-136-743B-58 Sequence 58, Appl
40 17 51.5 7 1 US-08-136-743B-59 Sequence 59, Appl
41 17 51.5 7 1 US-08-136-743B-60 Sequence 60, Appl
42 17 51.5 7 1 US-08-175-471-2 Sequence 2, Appli
43 17 51.5 7 2 US-08-429-054A-2 Sequence 2, Appli
44 17 51.5 7 2 US-08-718-777-2 Sequence 2, Appli
45 17 51.5 7 3 US-09-040-216-3 Sequence 3, Appli

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ALIGNMENTS

```

RESULT 1
US-08-222-619-8
; Sequence 8, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-222-619-8

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Query Match 72.7%; Score 24; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FTLEISR 7
   |||||
Db 1 FTFEYSR 7

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RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:

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; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04075-8

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 71.4%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 1 FTFEYSR 7

RESULT 3
US-09-423-468A-6
; Sequence 6, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Brassica oleracea
US-09-423-468A-6

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEISR 7
Db 2 TLELSK 7

RESULT 4
US-08-222-619-21
; Sequence 21, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-222-619-21

Query Match 57.6%; Score 19; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEIS 6
Db 1 FTFEYS 6

RESULT 5
PCT-US95-04075-21
; Sequence 21, Application PC/TUS9504075
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04075
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: peptide
PCT-US95-04075-21
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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04075-21

Query Match      57.6%; Score 19; DB 5; Length 6;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
Db 1 FTFEYS 6

RESULT 6
US-08-136-743B-55
; Sequence 55, Application US/08136743B
; Patent No. 5459063
; GENERAL INFORMATION:
; APPLICANT: Barry S. Cooperman, Harvey Rubin,
; APPLICANT: Jerome Salem, and Alison L. Fisher
; TITLE OF INVENTION: "plasmodium falciparum Ribonu-
; TITLE OF INVENTION: cleotide Reductase, DNA Sequences Therefor and Peptide inhibi-
; TITLE OF INVENTION: thereof"
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The University of Pennsylvania
; STREET: Suite 330
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19104-3246
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,743B
; FILING DATE: 10/14/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 3957-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELEX: No. 5459063e
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-136-743B-55

Query Match      57.6%; Score 19; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEI 5
Db 1 FTLDL 5

RESULT 7
US-09-040-216-28
; Sequence 28, Application US/09040216
; Patent No. 6030942
; GENERAL INFORMATION:
; APPLICANT: COOPERMAN, ET AL., BARRY
; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
; TITLE OF INVENTION: SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF

```

```

; TITLE OF INVENTION: RIBONUCLEOTIDE REDUCTASE
; FILE REFERENCE: 9596-6301
; CURRENT APPLICATION NUMBER: US/09/040,216
; CURRENT FILING DATE: 1998-03-17
; EARLIER APPLICATION NUMBER: 08/919,748
; EARLIER FILING DATE: 1997-08-28
; EARLIER APPLICATION NUMBER: 60/025,146
; EARLIER FILING DATE: 1996-08-30
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Ribonucleotide reductase inhibitor peptide
; FEATURE:
; OTHER INFORMATION: residue 1: MOD_RES: ACETYLATION
US-09-040-216-28

Query Match      57.6%; Score 19; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEI 5
Db 1 FTLDL 5

RESULT 8
US-08-297-731-4
; Sequence 4, Application US/08297731
; Patent No. 5574008
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Wadus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,731
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-297-731-4

Query Match      54.5%; Score 18; DB 1; Length 6;

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-332A-6
Query Match      54.5%; Score 18; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
   || :||
Db 1 FTSDVS 6

RESULT 9
US-09-623-618B-6
; Sequence 6, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001620
; CURRENT APPLICATION NUMBER: US/09/623,618B
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-618B-6
Query Match      54.5%; Score 18; DB 3; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
   || :||
Db 1 FTSDVS 6

RESULT 10
US-09-657-332A-6
; Sequence 6, Application US/09657332A
; Patent No. 6514500
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)
; FILE REFERENCE: 500862001600
; CURRENT APPLICATION NUMBER: US/09/657,332A
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-876-388-6
Query Match      54.5%; Score 18; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
   || :||
Db 1 FTSDVS 6

RESULT 11
US-09-876-388-6
; Sequence 6, Application US/09876388
; Patent No. 6593295
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001610
; CURRENT APPLICATION NUMBER: US/09/876,388
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/623,618
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-876-388-6
Query Match      54.5%; Score 18; DB 4; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEIS 6
   || :||
Db 1 FTSDVS 6

RESULT 12
PCT-US95-10793-4
; Sequence 4, Application PC/TUS9510793
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Madus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
```

```
;
;
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10793
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-10793-4

Query Match 54.5%; Score 18; DB 5; Length 6;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
   ||::|
Db 1 FTSDVS 6

RESULT 13
; Sequence 5, Application US/08297731
; Patent No. 5574008
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; APPLICANT: Yakubu-Madus, Fatima E.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,731
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Maciak, Ronald S.
; REGISTRATION NUMBER: 35,262
; REFERENCE/DOCKET NUMBER: X9630
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-1664
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-297-731-5
; Query Match 54.5%; Score 18; DB 3; Length 7;
; Best Local Similarity 50.0%; Pred. No. 3.8e+05;
; Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
   ||::|
Db 2 FTSDVS 7

RESULT 14
; US-09-623-618B-7
; Sequence 7, Application US/09623618B
; Patent No. 6329336
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.
; APPLICANT: L'Archeveque, Benoit
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Holmes, Darren L.
; APPLICANT: Leblanc, Anouk
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 500862001620
; CURRENT APPLICATION NUMBER: US/09/623.618B
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13563
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-09-623-618B-7

Query Match 54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEIS 6
   ||::|
Db 2 FTSDVS 7

RESULT 15
; US-09-218-363-23
; Sequence 23, Application US/09218363
; Patent No. 6387616
; GENERAL INFORMATION:
; APPLICANT: Ozelius, Laurie J.
; APPLICANT: Breakfield, Xandra O.
; TITLE OF INVENTION: TORSIN, TORSIN GENES, AND METHODS OF USE
; FILE REFERENCE: MGH-1184pa2
; CURRENT APPLICATION NUMBER: US/09/218,363
; CURRENT FILING DATE: 1998-12-22
; EARLIER APPLICATION NUMBER: 09/099,454
; EARLIER FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 60/050,244
; EARLIER FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 7
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us-09-712-819d-12.closed.ra1

Thu Nov 4 07:26:49 2004

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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-218-363-23
Query Match      54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLE 4
        |||.
Db      2 FTME 5

Search completed: November 4, 2004, 01:25:35
Job time : 24.6667 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	13	39.4	6	2 B26206	alpha-1,4-glucan-p
2	13	39.4	7	2 E48394	Glycoprotein compo
3	13	39.4	7	2 I48086	DNA topoisomerase
4	13	39.4	7	2 E48394	major fat-globule
5	12	36.4	5	2 T14910	hypothetical prote
6	11	33.3	4	2 A61300	22K superhelical D
7	11	33.3	5	2 PT0644	T-cell receptor be
8	11	33.3	7	2 S19630	ribosomal protein
9	10	30.3	5	2 A60521	glycogen phosphory
10	10	30.3	7	2 B39127	phosphotransferase
11	10	30.3	7	2 PS0254	18K protein 5507 -
12	10	30.3	7	2 S33244	neuromodulatory pe
13	10	30.3	7	2 S33245	neuromodulatory pe
14	9	27.3	3	2 T13892	cytochrome-c oxida
15	9	27.3	5	2 A44955	alkanal monooxygen
16	9	27.3	5	2 S11127	phosphoprotein, bo
17	9	27.3	5	2 PT0525	T-cell receptor be
18	9	27.3	5	2 PT0577	T-cell receptor be
19	9	27.3	5	2 PT0700	T-cell receptor be
20	9	27.3	5	2 S69237	surface protein te
21	9	27.3	5	2 E42364	flagellar protein
22	9	27.3	5	2 PT0565	T-cell receptor be
23	9	27.3	6	2 B34835	dnaA protein - pse
24	9	27.3	6	2 A60986	N-formyl oligopept
25	9	27.3	6	2 T11779	phosphoglycerate t
26	9	27.3	6	2 A43766	28K ubiquitin-immu
27	9	27.3	6	2 JH0784	neuropeptide TE-6
28	9	27.3	6	2 I37263	Y protein - human
29	9	27.3	6	2 S78764	ribosomal protein

30 fatty-acid synthas
31 MHC H2-L antigen -
32 T-cell receptor be
33 T-cell receptor be
34 peptidyl-dipeptida
35 piiz protein - Esc
36 phosphonoacetaldeh
37 omega-gliadine 1,
38 ig heavy chain CSD
39 ig kappa chain V-I
40 T-cell receptor be
41 peptidylglycine mo
42 carnosin UI49 - Ca
43 pullulanase (EC 3.
44 choline oxidase (E
45

ALIGNMENTS

RESULT 1

B26206
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C:Accession: B26206; A26206
R:Larner, J.; Sanger, F.
J. Mol. Biol. 11, 491-500, 1965

A:Title: The amino acid sequence of the phosphorylation site of muscle uridine diphosph
A:Reference number: A26206
A:Accession: B26206
A:Molecule type: protein
A:Residues: 1-6 <IAR>
A:Experimental source: muscle
A:Note: Lys-1 was also found
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;4/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6

Db 2 EIS 4

RESULT 2

E48394

Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: E48394

R:Mathier, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993

A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig

II-like sequences.

A:Reference number: A48394; PMID:8485470

A:Accession: E48394

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MAP>

A:Experimental source: milk

A:Note: sequence extracted from NCBI backbone (NCBIP:131450)

C:Keywords: glycoprotein

Query Match 39.4%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 EISR 7

|||

Db	4	ELAR 7	Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
RESULT 3			
I48086			
DNA topoisomerase II alpha - Chinese hamster (fragment)			
C:Species: Cricetulus griseus (Chinese hamster)			
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999			
C:Accession: I48086			
R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.			
J. Biol. Chem. 270, 25850-25858, 1995			
A:Title: Molecular cloning and characterization of the promoter for the Chinese hamster			
A:Reference number: I48086; MUID:96029684; PMID:7592770			
A:Accession: I48086			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: DNA			
A:Residues: 1-7 <RES>			
A:Cross-references: EMBL:U34196; NID:gl041231; PID:g1041232			
Query Match 39.4%; Score 13; DB 2; Length 7;			
Best Local Similarity 50.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
Qy	3	LEIS 6	
	:	:	
Db	1	MELS 4	
RESULT 4			
B48394			
major fat-globule membrane protein GP 55 - guinea pig (fragment)			
C:Species: Cavia porcellus (guinea pig)			
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995			
C:Accession: B48394			
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.			
Biochem. Mol. Biol. Int. 29, 545-554, 1993			
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig			
ii-like sequences.			
A:Reference number: A48394; MUID:93250576; PMID:8485470			
A:Accession: B48394			
A>Status: preliminary			
A:Molecule type: protein			
A:Residues: 1-7 <MR>			
A:Experimental source: milk			
A>Note: sequence extracted from NCBI backbone (NCBIP:131444)			
Query Match 39.4%; Score 13; DB 2; Length 7;			
Best Local Similarity 50.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
Qy	4	EISR 7	
	:	:	
Db	4	ELAR 7	
RESULT 5			
T14910			
hypothetical protein - parsley			
C:Species: Petroselinum crispum (parsley)			
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000			
C:Accession: T14910			
R:Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.			
Mol. Gen. Genet. 257, 595-605, 1998			
A:Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of			
A:Reference number: Z18261; MUID:98265918; PMID:9604882			
A:Accession: T14910			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-5 <KR>			
A:Cross-references: EMBL:Y10810; NID:g33336904; PIDN:CAA71769.1; PID:g33336905			
A:Experimental source: ssp. Hamburger Schnitt			
Query Match 36.4%; Score 12; DB 2; Length 5;			
RESULT 6			
A61300			
22K superhelical DNA-binding protein - Escherichia coli (fragment)			
C:Species: Escherichia coli			
C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999			
C:Accession: A61300			
R:Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.			
J. Biochem. 92, 1059-1063, 1982			
A:Title: Purification and characterization of a protein from Escherichia coli which for			
A:Reference number: A61300; MUID:83082696; PMID:6294066			
A:Accession: A61300			
A:Molecule type: protein			
A:Residues: 1-4 <KIS>			
C:Comment: This protein resembles some of the histone-like protein of bacteria in amino			
C:Keywords: DNA binding; monomer			
Query Match 33.3%; Score 11; DB 2; Length 4;			
Best Local Similarity 66.7%; Pred. No. 2.8e+05;			
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	3	LEI 5	
	:	:	
Db	1	MEI 3	
RESULT 7			
PT0644			
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)			
C:Species: Mus musculus (house mouse)			
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004			
C:Accession: PT0644			
R:Feeney, A.J.			
J. Exp. Med. 174, 115-124, 1991			
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.			
A:Reference number: PT0509; MUID:91277601; PMID:1711558			
A:Accession: PT0644			
A>Status: translation not shown			
A:Molecule type: mRNA			
A:Residues: 1-5 <FEE>			
A:Cross-references: UNIPROT:Q9Z2T6			
A:Experimental source: newborn thymus, strain BALB/c			
C:Keywords: T-cell receptor			
Query Match 33.3%; Score 11; DB 2; Length 5;			
Best Local Similarity 100.0%; Pred. No. 2.8e+05;			
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	FT 2	
	:	:	
Db	4	FT 5	
RESULT 8			
S19630			
ribosomal protein L30 - Streptomyces griseus (fragment)			
C:Species: Streptomyces griseus			
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997			
C:Accession: S19630			
R:Ochi, K.			
Int. J. Syst. Bacteriol. 42, 144-150, 1992			
A:Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete			
A:Reference number: S19630; MUID:92144363; PMID:1736962			
A:Accession: S19630			
A:Molecule type: protein			
A:Residues: 1-7 <OCH>			

A;Experimental source: strain IFO 13189
C;Superfamily: Escherichia coli ribosomal protein L30
C;Keywords: protein biosynthesis; ribosome

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEISR 7
|:|:
Db 3 LKITQ 7

RESULT 9

A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A;Reference number: A60521; MUID:90227907; PMID:2109669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 30.3%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
|:|:
Db 1 QIS 3

RESULT 10

B39127
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C;Accession: B39127
R;Hardisty, C.; Ferran, C.; Di Rienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A;Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sd
in.

A;Reference number: A39127; MUID:91100329; PMID:1846143
A;Accession: B39127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <HAR>
A;Cross-references: GB:M38416; NID:G155142; PIDN:AAA98418.1; PID:G155144
C;Keywords: phosphotransferase

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
|:|:
Db 5 QIS 7

RESULT 11

PS0254
18K protein 5507 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C;Accession: PS0254
R;Tsugita, A.

submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0254
A;Molecule type: protein
A;Residues: 1-7 <TSU>
A;Experimental source: leaf, chloroplast, strain Nihonbare
A;Note: molecular weight 18K, pI 4.4

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEISR 7
|:|:
Db 1 LAIAK 5

RESULT 12

S33244
neuromodulatory peptide WWamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33244
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33244
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
A;Cross-references: UNIPROT:P35921

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
|:|:
Db 3 EMS 5

RESULT 13

S33245
neuromodulatory peptide WWamide-2 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33245
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
A;Cross-references: UNIPROT:P35919

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
|:|:
Db 3 EMS 5

RESULT 14

T13892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892

Thu Nov 4 07:26:50 2004

R;Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: T13892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
Db 2 TL 3

RESULT 15
A44955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment
C;Species: Vibrio harveyi
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquette, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
A;Reference number: A44955; MUID:90175700; PMID:2626493
A;Accession: A44955
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
||
Db 3 IXR 5

Search completed: November 4, 2004, 01:24:17
Job time : 18.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 Seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	14	42.4	7	2	P83530	lactobacill
2	13	39.4	6	1	U06_CLOPA	clostridium
3	13	39.4	6	2	P82181	spinacia ol
4	13	39.4	6	2	P82182	spinacia ol
5	11	33.3	5	1	RE31_LITRU	litoria rub
6	11	33.3	5	1	RE32_LITRU	litoria rub
7	10	30.3	7	1	E105_LITRU	litoria rub
8	10	30.3	7	1	WWA1_ACHF	achatina fu
9	10	30.3	7	1	WWA3_ACHF	achatina fu
10	9	27.3	5	1	UF01_MOUSE	mus musculu
11	9	27.3	7	1	CCF1_ENTFA	enterococcu
12	9	27.3	7	1	CHOX_ALGSP	alcaligenes
13	9	27.3	7	1	CIA_ENTFA	enterococcu
14	9	27.3	7	1	GFRP_MOUSE	mus musculu
15	9	27.3	7	1	LANC_CARUI	carnobacter
16	9	27.3	7	2	P93233	lycopersico
17	9	27.3	7	2	O07354	synchococc
18	9	27.3	7	2	O0J881	human immu
19	8	24.2	5	1	ALL14_CARMA	carcinus ma
20	8	24.2	5	1	PSK_DAUCA	carcinus ma
21	8	24.2	5	1	UC22_MAIZE	daucus caro
22	8	24.2	7	1	ALL2_CARMA	zea mays (m
23	8	24.2	7	1	ALL3_CARMA	carcinus ma
24	8	24.2	7	1	ALL4_CARMA	carcinus ma
25	8	24.2	7	1	ALL5_CARMA	carcinus ma
26	8	24.2	7	1	ALL7_CYPDO	cydia pomon
27	8	24.2	7	1	FAR1_ASCSU	ascaris suu
28	8	24.2	7	2	Q15903	homo sapien
29	8	24.2	7	2	Q8TRAQ4	homo sapien
30	8	24.2	7	2	P70804	azotobacter
31	8	24.2	7	2	Q9YIQ9	human adeno

32 8 24.2 7 2 Q9YI0 human adeno
33 8 24.2 7 2 Q9YI0 human adeno
34 8 24.2 7 2 Q9YI0 human adeno
35 8 24.2 7 2 Q9YI0 human adeno
36 7 21.2 4 1 ILME_SEPOF
37 7 21.2 5 1 RE21_LITRU
38 7 21.2 6 1 ACPH_RABIT
39 7 21.2 6 1 LOK1_LOCOMI
40 7 21.2 6 2 P82541
41 7 21.2 7 1 FAR2_ASCSU
42 7 21.2 7 1 UF03_MOUSE
43 7 21.2 7 1 WWA2_ACHF
44 7 21.2 7 2 Q15837
45 7 21.2 7 2 Q95945

ALIGNMENTS

RESULT 1

P83530 ID P83530 PRELIMINARY; PRT; 7 AA.
AC P83530;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
OS Unknown protein from 2D-page (Fragment).
OC Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -|- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
protein is: 15 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 42.4%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLEI 5
Db 2 TLDV 5

RESULT 2

U06_CLOPA ID U06_CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";

```
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
KW Direct protein sequencing.
FT NON_TER 6
SQ SEQUENCE 6 AA; 657 MW; 605BD1CIA45A8000 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLEI 5
DB 3 TAEI 6

RESULT 3
P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:RNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
DB 2 ISR 4

RESULT 5
RE31_LITRU STANDARD; PRT; 5 AA.
ID RE31_LITRU
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CH10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
DB 4 FT 5

RESULT 6
RE32_LITRU
```

```
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.0, its MW is: 75.9 kDa.
KW Direct protein sequencing.
FT NON_TER 6
SQ SEQUENCE 6 AA; 657 MW; 605BD1CIA45A8000 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLEI 5
DB 3 TAEI 6

RESULT 3
P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:RNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
DB 2 ISR 4

RESULT 5
RE31_LITRU STANDARD; PRT; 5 AA.
ID RE31_LITRU
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CH10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
DB 4 FT 5

RESULT 6
RE32_LITRU
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ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db |||
4 FT 5

RESULT 7
ID_EI05_LITRU STANDARD; PRT; 7 AA.
AC P82101;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 5.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076B0B5030 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db |||
5 EIA 7

RESULT 8
ID_WWAL_ACHFU STANDARD; PRT; 5 AA.
DT 01-OCT-1994 (Rel. 30, Created)

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ID WWAL_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: Exhibits modulatory effects on the peripheral nervous
CC system. Inhibits activity on a central neuron.
DR PIR; S33245; S33245.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db |||
3 EMS 5

RESULT 9
ID_WWAL_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RA MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EIS 6
Db |||
3 EMS 5

RESULT 10
ID_UF01_MOUSE STANDARD; PRT; 5 AA.
DT 01-OCT-1994 (Rel. 30, Created)

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DT	01-OCT-1994 (Rel. 30, Last sequence update)	OS	Alcaligenes sp.
DT	05-JUL-2004 (Rel. 44, Last annotation update)	OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
DE	Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).	OC	Alcaligenaceae; Alcaligenes.
OS	Mus musculus (Mouse).	OX	NCBI_TaxID=512;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RP	[1]
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	RP	SEQUENCE.
OX	NCBI_TaxID=10090;	RX	MEDLINE=81006769; PubMed=6997283;
RP	[1]	RX	Medline=95009907; Wichter L.L., He C., Selkirk J.K.;
RP	TISSUE=Fibroblast;	RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RC	MEDLINE=95009907; PubMed=7523108;	RA	"Separation and sequencing of familial and novel murine proteins using
RA	Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;	RT	preparative two-dimensional gel electrophoresis.";
RT	"Separation and sequencing of familial and novel murine proteins using	RT	Electrophoresis 15:735-745(1994).
RT	preparative two-dimensional gel electrophoresis.";	RL	Electrophoresis 15:735-745(1994).
RL	Electrophoresis 15:735-745(1994).	CC	-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC	protein is: 6.6, its MW is: 19 kDa.	CC	protein is: 6.6, its MW is: 19 kDa.
CC	Direct protein sequencing.	KW	Direct protein sequencing.
KW	Direct protein sequencing.	FT	NON_TER
FT	NON_TER	FT	NON_TER
SQ	SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;	SQ	SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;
Query Match 27.3%; Score 9; DB 1; Length 5;			
Best Local Similarity 66.7%; Pred. No. 1.8e+06;			
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	5 ISR 7	QY	6 SR 7
DB	2 IGR 4	DB	6 SR 7
RESULT 11			
ID	CCFI_ENTFA	ID	CIA_ENTFA
AC	P20104;	AC	P11932;
DT	01-FEB-1991 (Rel. 17, Created)	DT	01-OCT-1989 (Rel. 12, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)	DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Sex pheromone cCF10.	DE	Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS	Enterococcus faecalis (Streptococcus faecalis).	OS	Enterococcus faecalis (Streptococcus faecalis).
OC	Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.	OC	Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX	NCBI_TaxID=1351;	OX	NCBI_TaxID=1351;
RN	[1]	RN	[1]
RP	SEQUENCE.	RP	SEQUENCE.
RX	MEDLINE=89008313; PubMed=3139658;	RX	MEDLINE=87005252; PubMed=3093276;
RA	Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,	RA	Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA	Adsit J.C., Dunny G.M., Suzuki A.;	RA	White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT	"Structure of cCF10, a peptide sex pheromone which induces conjugative	RT	"Isolation and structure of the Streptococcus faecalis sex pheromone,
RT	transfer of the Streptococcus faecalis tetracycline resistance	RT	CAM373.";
RT	plasmid, pCF10.";	RL	FEBS Lett. 206:69-72(1986).
RL	J. Biol. Chem. 263:14574-14578(1988).	CC	-!- FUNCTION: CAM373 induces mating response of donor cells harboring
CC	-!- FUNCTION: cCF10 is involved in the conjugative transfer of the	CC	PAM373.
CC	hemolysin plasmid pCF10.	CC	-!- MISCELLANEOUS: The N-terminus is possibly responsible for
KW	Direct protein sequencing; Pheromone.	KW	Direct protein sequencing; Pheromone.
PIR	A30812; A30812.	PIR	A25269; A25269.
SQ	SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;	SQ	SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
Query Match 27.3%; Score 9; DB 1; Length 7;			
Best Local Similarity 100.0%; Pred. No. 1.8e+06;			
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	2 TL 3	QY	1 FTL 3
DB	3 TL 4	DB	3 FIL 5
RESULT 12			
ID	CHOX_ALCSP	ID	GRFP_MOUSE
AC	P16101;	AC	P99025;
DT	01-APR-1990 (Rel. 14, Created)	DT	15-DEC-1998 (Rel. 37, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)	DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)	DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Choline oxidase (EC 1.1.3.17) (Fragment).	DE	GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN	Name=Gchfr; Synonyms=Gfrp;	GN	Name=Gchfr; Synonyms=Gfrp;
OS	Mus musculus (Mouse).	OS	Mus musculus (Mouse).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
 RL Submitted (AUG-1998) to Swiss-Prot.
 CC -!- FUNCTION: Mediates tetrahydropterin inhibition of GTP
 CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
 CC (By similarity).
 CC -!- SUBUNIT: Homodimer (By similarity).
 DR SWISS-2DPAGE; P99025; MOUSE.
 KW Direct protein sequencing.
 FT INIT MET 0
 FT NON TER 7
 SQ SEQUENCE 7 AA; 806 MW; 71B5B05723B4700 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEIS 6
 Db 3 LLIS 6

RESULT 15
 LANC CARUI STANDARD; PRT; 7 AA.
 AC F36960;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lantibiotic carnocin UI49 (Fragment).
 OS Carnobacterium sp. (strain UI49).
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
 OC Carnobacterium.
 OX NCBI_TaxID=35782;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92321768; PubMed=1622206;
 RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
 RA Nes I.F.;
 RT "Purification and characterization of a new bacteriocin isolated from
 a Carnobacterium sp.";
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).
 CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
 CC Active on Gram-positive bacteria.
 KW Antibiotic; Bacteriocin; Direct protein sequencing; Lantibiotic.
 FT NON TER 7
 SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EI 5
 Db 3 EI 4

Search completed: November 4, 2004, 01:23:17
 Job time : 100.667 secs

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CC protein can be used to ameliorate ischaemia-reperfusion injury,
 CC rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma
 CC substances released after inflammation, etc

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 2; Length 7;
 Best Local Similarity 71.4%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 :|||
 Db 1 FTFEYSR 7

RESULT 2
 AAY41889
 ID AAY41889 standard; peptide; 7 AA.

XX AC AAY41889;
 XX 09-DEC-1999 (first entry)
 DT DE Rheumatoid arthritis diagnostic protein isoform peptide #40.
 XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADP; detection;
 KW rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
 KW rheumatoid arthritis diagnostic protein isoform; screening;
 KW expression reference protein isoform; prognosis.

XX OS Homo sapiens.
 XX WO9947925-A2.
 PN 23-SEP-1999.
 PD 15-MAR-1999; 99WO-GB000763.
 PF 13-MAR-1998; 98GB-00005477.

PR (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Parekh RB, Patel TP, Townsend RR;
 PI WPI; 1999-571871/48.
 DR Diagnosis of human rheumatoid arthritis by two-dimensional
 PT electrophoresis.
 PS Disclosure; Page 18; 157pp; English.

CC A method has been developed for the diagnosis of human rheumatoid
 CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
 CC dimensional array of features. The method can be used for screening,
 CC diagnosis and prognosis of RA in a subject or for monitoring the effect
 CC of an anti-RA drug or therapy administered to a subject. The method
 CC comprises: (a) analysing a sample of serum or plasma and optionally
 CC synovial fluid by two-dimensional electrophoresis, to generate a two-
 CC dimensional array of features; (b) identifying at least one chosen
 CC feature whose relative abundance correlates with the presence or absence
 CC of RA; and (c) comparing the abundance of each chosen feature in the
 CC sample with the abundance of that chosen feature in serum or plasma from
 CC one or more persons without RA, where the relative abundance of the
 CC chosen feature or features in the sample indicates the presence or
 CC absence of RA in the subject. The method can also be used in clinical
 CC studies for testing drugs for therapy of RA, for purification of RA-
 CC diagnostic protein isoforms (RPIs), and for production of antibodies to
 CC RPIs. The RA-diagnostic feature (RADP) proteins can be used to identify
 CC compounds that promote or inhibit their activity, which are then used as
 CC RA drugs. Nucleic acid encoding RADPs can be used in gene therapy
 CC protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
 CC AAY42103 represent expression reference protein isoform peptides and
 CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all

CC used in the exemplification of the present invention
 XX Sequence 7 AA;

Query Match 72.7%; Score 24; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 :|||
 Db 1 VTFELSR 7

RESULT 3
 ABB55870
 ID ABB55870 standard; peptide; 7 AA.

XX AC ABB55870;
 XX 15-FEB-2002 (first entry)
 DT DE Vascular dementia-associated protein isoform (VPI) 70.
 XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.

XX OS Homo sapiens.
 XX WO200169261-A2.
 PN 20-SEP-2001.
 PD 14-MAR-2001; 2001WO-GB001106.
 PF 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA Herath IMAC, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.

DR Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy, for
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.

PS Claim 6; Page 31; 151pp; English.

CC The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7

XX OS Homo sapiens.
 XX PN WO200162787-A1.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000786.
 XX PR 24-FEB-2000; 2000GB-00004412.
 XX PR 08-DEC-2000; 2000GB-00030050.
 XX PR 12-DEC-2000; 2000US-0254830P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX DR WPI; 2001-570626/64.
 XX PT Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
 XX PS Disclosure; Page 34; 153pp; English.
 XX CC The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), manic-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present invention
 XX DT Sequence 7 AA;
 XX DE Query Match 72.7%; Score 24; DB 4; Length 7;
 XX DE Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 XX DE Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLEISR 7
 DB :||:|
 1 YTFELSR 7
 RESULT 7
 AAU24969
 ID AAU24969 standard; peptide; 7 AA.
 AC AAU24969;
 XX DT 18-DEC-2001 (first entry)
 XX DE Depression-Associated Protein Isoform (SPI) peptide #198.
 XX DE Schizophrenia-Associated Protein Isoform (SPI) peptide #198.
 XX DE Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
 XX OS Homo sapiens.
 XX PN WO200162785-A2.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000792.
 XX PR 24-FEB-2000; 2000GB-00004415.

PR 28-DEC-2000; 2000US-00750395.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMCAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;
 XX DR WPI; 2001-570624/64.
 XX PT New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
 XX PS Disclosure; Page 32; 148pp; English.
 XX CC The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
 XX DT Sequence 7 AA;
 XX DE Query Match 72.7%; Score 24; DB 4; Length 7;
 XX DE Best Local Similarity 57.1%; Pred. No. 1.7e+06;
 XX DE Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLEISR 7
 DB :||:|
 1 YTFELSR 7
 RESULT 8
 AAU26249
 ID AAU26249 standard; peptide; 7 AA.
 AC AAU26249;
 XX DT 18-DEC-2001 (first entry)
 XX DE Depression-Associated Protein isoform DPI-208.
 XX DE Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
 XX DE DPI; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
 XX DE CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 XX DE attention deficient disorder; schizoaffective disorder;
 XX DE unipolar affective disorder.
 XX OS Homo sapiens.
 XX PN WO200163294-A2.
 XX PD 30-AUG-2001.
 XX PF 23-FEB-2001; 2001WO-GB000791.
 XX PR 24-FEB-2000; 2000GB-00004412.
 XX PR 08-DEC-2000; 2000GB-00030050.
 XX PR 12-DEC-2000; 2000US-0254830P.
 XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX PI Herath HMCAC, Parekh RB, Rohlf C;
 XX DR WPI; 2001-582081/65.
 XX PT Preparation for diagnosing or treating bipolar affected disorder (BAD) or unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
 XX PS Claim 8; Page 34; 163pp; English.

XX The invention relates to a preparation comprising an isolated Bipolar
CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
CC used to screen, diagnose or prognosis of BAD or unipolar depression,
CC determine the stage or severity of BAD or unipolar depression, identify a
CC subject at risk of developing BAD or unipolar depression, or monitor the
CC effect of therapy in a subject. They are also used to screen for or
CC identify agents that interact with a DPI. These agents, antibodies
CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
CC or prevent BAD or unipolar depression. Diseases that can be treated are
CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
CC unipolar affective disorder. The DPIs are used in proteomics. The
CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
CC BAD or unipolar depression overcomes the problems of using gene
CC expression analysis, such as not being able to obtain central nervous
CC system (CNS) tissue from a living patient under normal circumstances. The
CC present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
CC subjects having BAD
XX

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 9
AAU15313
ID AAU15313 standard; peptide; 7 AA.
XX
AC AAU15313;
XX

DT 24-OCT-2001 (first entry)
XX

DE Schizophrenia-associated isoform peptide #198.
XX

KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
KW neurological disorder; neuropathy.
XX

OS Homo sapiens.
XX

PN WO200163293-A2.
XX

PD 30-AUG-2001.
XX

PF 23-FEB-2001; 2001WO-GB000783.
XX

PR 24-FEB-2000; 2000GB-00004415.
XX

PR 28-DEC-2000; 2000US-00750395.
XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX

PI Herath HMAc, Parekh RB, Rohlf C;
XX

PI WPI; 2001-502868/55.
XX

DR Diagnosing and monitoring Schizophrenia by detecting the presence of
PT Schizophrenia Associated Features and Schizophrenia Associated Protein
PT Isoforms in samples of cerebrospinal fluid.
XX

PS Claim 6; Page 32; 160pp; English.
XX

XX The invention relates to methods for screening,
CC diagnosis and prognosis of Schizophrenia. The method involves detecting
CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
CC immun assay or hybridisation assay, for diagnosing and monitoring SCH,
CC studying the effectiveness of treatments and for identifying potential
CC therapeutic agents. The method is used for (1) screening or diagnosis of

CC SCH and the relative abundance of at least 1 chosen feature correlates
CC with the presence or absence of SCH; and (2) monitoring the effect of
CC therapy administered to a subject with SCH and the relative abundance of
CC at least 1 chosen feature which correlates with the severity of SCH. The
CC expression and activity of the SFs, SPIs and related molecules (e.g.
CC secondary messengers) are studied to diagnose SCH, monitor the progress
CC of the disorder and the effectiveness of treatment and as targets to
CC identify and produce potential therapeutic agents for the treatment of
CC SCH. The paucity of detectable neuronal defects distinguishes
CC neuropsychiatric disorders such as SCH from neurological disorders, where
CC manifestations of anatomical and biochemical changes have been identified
CC in many cases. Consequently the identification and characterisation of
CC cellular and/or molecular causative defects and neuropathies are
CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-
CC AAU15762 represent the amino acid sequences of schizophrenia-associated
CC isoforms used in the method of the invention
XX

SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 10
ABBS2190
ID ABBS2190 standard; peptide; 7 AA.
XX
AC ABBS2190;
XX

DT 08-FEB-2002 (first entry)
XX

DE Human API-146 tryptic digest peptide #1.
XX

KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX

OS Homo sapiens.
XX

PN WO200175454-A2.
XX

PD 11-OCT-2001.
XX

PF 03-APR-2001; 2001WO-US010908.
XX

PR 03-APR-2000; 2000US-0194504P.
XX

PR 28-NOV-2000; 2000US-0253647P.
XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX

PA (PFIZ) PFIZER INC.
XX

PI Durham KL, Friedman DL, Herath HMAc, Kimmel LH, Parekh RB;
PI Potter KM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX

PI WPI; 2001-639384/73.
XX

PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX

PS Example; Page 30; 162pp; English.
XX

XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or

CC plasma. The abundance of the Afs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the Afs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 1 YTFEYSR 7

RESULT 11
ABB52355
ID ABB52355 standard; peptide; 7 AA.
XX AC ABB52355;
XX DT 08-FEB-2002 (first entry)
XX Human API-125 tryptic digest peptide #9.
XX Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX OS Homo sapiens.
XX WO200175454-A2.
XX PD 11-OCT-2001.
XX PF 03-APR-2001; 2001WO-US010908.
XX PR 03-APR-2000; 2000US-0194504P.
XX PR 28-NOV-2000; 2000US-0253647P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX Durham KL, Friedman DL, Herath HM, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX WPI; 2001-639384/73.
XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
XX array of a feature whose relative abundance correlates with disease, and
XX comparing with abundance of the feature in samples of healthy persons.
XX Example; Page 34; 162pp; English.
XX The invention relates to methods for the screening, diagnosis and
XX prognosis of Alzheimer's disease. The methods involve the detection of
XX Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
XX Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
XX plasma. The abundance of the Afs and APIs is then normalised to an
XX Expression Reference Protein Isoform (ERPI) in order to determine whether
XX a patient is suffering from, or has a predisposition to, Alzheimer's
XX Disease. The relative abundance of the Afs and APIs correlates with the
XX severity of Alzheimer's Disease. The present sequence is a peptide
XX produced from an API by proteolysis
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 1 YTFEYSR 7

RESULT 12
ABG78901
ID ABG78901 standard; peptide; 7 AA.
XX AC ABG78901;
XX DT 29-NOV-2002 (first entry)
XX Multiple sclerosis associated feature (MSF) tryptic digest peptide #389.
XX Multiple sclerosis; MS; multiple sclerosis associated feature; MSF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX OS Homo sapiens.
XX WO200259604-A2.
XX PD 01-AUG-2002.
XX PF 25-JAN-2002; 2002WO-GB000330.
XX PR 26-JAN-2001; 2001US-0264404P.
XX PR 20-NOV-2001; 2001US-0331647P.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX Herath HM, Parekh RB, Rohlf C;
XX WPI; 2002-599812/64.
XX Screening or diagnosing multiple sclerosis (MS), useful for e.g.
XX determining the stage or severity of MS, comprises detecting the presence
XX of MS-associated features or protein isoforms by 2-dimensional
XX electrophoresis.
XX Disclosure; Page 39; 128pp; English.
XX This invention relates to a novel method for screening or diagnosing
XX multiple sclerosis (MS) in a subject to determine the stage or severity
XX of MS, to identify a subject at risk of developing MS or to monitor the
XX effect of a therapy administered. The method comprises analysing a sample
XX body fluid from the subject by two-dimensional electrophoresis and
XX detecting the presence of multiple sclerosis-associated features (MSFs),
XX or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
XX the invention correspond to spots identified on a 2D gel these proteins
XX may have antiinflammatory or neuroprotective activity. The methods of the
XX invention and the compositions are useful for clinical screening,
XX diagnosis and treatment of MS, for monitoring the effectiveness of MS
XX treatment, for selecting participants in clinical trials, for identifying
XX patients most likely to respond to a particular therapeutic treatment and
XX for screening and developing drugs for treatment of MS. Agents that
XX modulate the expression or activity of an MSPI are useful for treating
XX MS, for preventing or delaying the onset or development of MS, to prevent
XX or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
XX acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
XX or their fragments are useful for promoting MSPI function by gene
XX therapy. The present sequence represents a human multiple sclerosis
XX associated feature tryptic digest peptide of the invention
XX
SQ Sequence 7 AA;

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 13
ABG78730
ID ABG78730 standard; peptide; 7 AA.
XX
AC ABG78730;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #218.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
EN
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB000330.
XX
PR 26-JAN-2001; 2001US-0264404P.
PR 20-NOV-2001; 2001US-0331647P.
XX
XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
PA
XX
PI Herath HMAc, Parekh RB, Rohlf C;
XX
XX WPI; 2002-599812/64.
DR
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence
PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
XX Disclosure; Page 26; 128pp; English.
XX
CC This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention
XX
XX Sequence 7 AA;

Query Match 72.7%; Score 24; DB 5; Length 7;
Best Local Similarity 57.1%; Pred No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

Db 1 YTFELSR 7
:|:|:
RESULT 14
ABP58010
ID ABP58010 standard; peptide; 7 AA.
XX
AC ABP58010;
XX
DT 11-FEB-2003 (first entry)
XX
DE Prostate cancer marker protein peptide fragment.
XX
KW Prostate cancer; marker; vitamin D binding protein; VDBP; human;
KW diagnosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200275314-A2.
XX
PD 26-SEP-2002.
XX
PF 30-NOV-2001; 2001WO-US045031.
XX
PR 30-NOV-2000; 2000US-0250284P.
PR 08-NOV-2001; 2001US-0344948P.
XX
XX (MATR-) MATRITECH INC.
XX
PI Hlavaty J, Briggman JV;
XX
XX WPI; 2003-067369/06.
DR
XX
PT Diagnosing or treating prostate cancer by detecting in a sample isolated
PT from the individual the presence of prostate cancer-associated protein.
XX
XX Claim 1; Page 41; 63pp; English.
XX
CC The present sequence is that of a peptide fragment of a novel human 50.8
CC kDa prostate cancer-associated protein that has been identified as a
CC highly effective marker for prostate cancer. The novel protein includes a
CC polypeptide that is related to human serum vitamin D binding protein
CC (VDBP; see ABP58017). The present peptide corresponds to amino acids 346-
CC 352 of this VDBP allele. It is one of a series of peptides (see ABP58005-
CC 16) that distinguish VDBP-related proteins from other proteins, or which
CC may be characterised as binding specifically to an anti-VDBP antibody.
CC VDBP-related proteins are detectable at a higher concentration in serum
CC from a mammal, e.g. a human, with prostate cancer relative to serum from
CC a healthy mammal and can therefore be used as prostate cancer markers.
CC They permit the rapid detection, preferably before metastases occur, of
CC prostate cancer. A target prostate cancer-associated protein may be
CC detected using a labelled antibody capable of binding specifically to the
CC protein. Prostate cancer-associated proteins, and nucleic acids encoding
CC them, are also useful as targets for treating prostate cancer, and as
CC indicators for monitoring the efficiency of prostate cancer therapy
XX
XX Sequence 7 AA;

Query Match 72.7%; Score 24; DB 6; Length 7;
Best Local Similarity 57.1%; Pred No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLEISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 15
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ID ABP57255 standard; peptide; 7 AA.
XX
XX ABP57255;
AC

Search completed: November 4, 2004, 01:18:14
Job time : 94.3333 secs

XX 16-APR-2003 (first entry)
XX Breast cancer associated tryptic digest peptide SEQ ID NO:154.
DE Breast cancer associated feature; BF; BPI; breast cancer; diagnosis;
XX Breast cancer associated protein isoform; cytostatic; gene therapy.
KW
XX Homo sapiens.
OS Synthetic.
OS
XX WC200288750-A2.
PN
XX
XX 07-NOV-2002.
PD
XX
XX 02-MAY-2002; 2002WO-GB002022.
PF
XX
XX 02-MAY-2001; 2001GB-00010790.
PR 27-JUL-2001; 2001GB-00018385.
PR 14-AUG-2001; 2001GB-00019791.
PR 16-AUG-2001; 2001GB-00020045.
PR 22-NOV-2001; 2001GB-00028062.
XX
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
XX Herath HMAC;
XX
XX WPI; 2003-175048/17.
XX
XX Screening, diagnosing or determining the stage or severity of breast
PT cancer, comprises analyzing and quantitatively detecting Breast Cancer-
PT Associated Features or Breast Cancer-Associated Protein Isoforms in a
PT biological sample.
XX
XX Example; Page 77; 88pp; English.
PS
XX The present invention describes a method for screening, diagnosing or
CC determining the stage or severity of breast cancer, identifying a subject
CC at risk of developing breast cancer, or monitoring the effect of therapy
CC administered to a subject with breast cancer, by generating a two-
CC dimensional array of features comprising breast cancer-associated
CC features (BPs). Or quantitatively detecting breast cancer-associated
CC protein isoforms (BPIs). Also described: (1) an antibody capable of
CC immunospecifically binding to one of the BPIs, (2) a pharmaceutical
CC compositions comprising: (a) a BPI, or a nucleic acid encoding a BPI, and
CC a carrier; or (b) the antibody of (1), or a fragment or derivative of the
CC antibody, and a carrier; (3) screening for agents that interact with one
CC or more BPIs, BPI fragments, polypeptides related to BPIs, or BPI-fusion
CC proteins; (4) screening for or identifying agents that modulate the
CC expression or activity of one or more BPIs, a BPI fragment, a BPI-related
CC polypeptide, or BPI-fusion proteins; and (5) treating or preventing
CC breast cancer. BPIs have cytostatic activity and can be used in gene
CC therapy. Methods and kits comprising antibodies or the BPIs from the
CC present invention can be used for screening, diagnosing or determining
CC the stage or severity of breast cancer, identifying a subject at risk of
CC developing breast cancer, or monitoring the effect of therapy
CC administered to a subject with breast cancer. The antibodies, BPIs,
CC nucleic acids encoding the BPIs, or an agent that modulates the activity
CC of one or more BPIs are useful for treating or preventing breast cancer.
CC ABP57104 to ABP57250 represent breast cancer associated tryptic digest
CC peptides, which are used in the exemplification of the present invention
XX
XX Sequence 7 AA;
SQ

Query Match 72.7%; Score 24; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 FTLEISR 7
Db 1 YTFELSR 7

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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 Seconds
(without alignments)
32.733 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues
Total number of hits satisfying chosen parameters: 56143

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	24	72.7	7	9	US-09-791-378-198
2	24	72.7	7	9	US-09-998-909-7
3	24	72.7	7	9	US-09-826-290-305
4	24	72.7	7	9	US-09-826-290-370
5	24	72.7	7	10	US-09-791-393-145
6	24	72.7	7	10	US-09-791-389-145
7	24	72.7	7	11	US-09-791-377-198
8	24	72.7	7	15	US-10-264-309-131
9	24	72.7	7	15	US-10-264-309-460
10	24	72.7	7	15	US-10-601-100-105
11	24	72.7	7	17	US-10-700-340-52
12	24	72.7	7	17	US-10-700-340-154
13	20	60.6	7	13	US-10-050-552A-4

14	20	60.6	7	14	US-10-234-026-6	Sequence 6, Appli
15	20	60.6	7	15	US-10-238-965-4	Sequence 4, Appli
16	18	54.5	5	16	US-10-803-622-3	Sequence 3, Appli
17	18	54.5	5	16	US-10-803-653-3	Sequence 3, Appli
18	18	54.5	6	9	US-09-876-388-6	Sequence 6, Appli
19	18	54.5	6	14	US-10-105-930-39	Sequence 39, Appli
20	18	54.5	6	14	US-10-287-892-6	Sequence 6, Appli
21	18	54.5	6	14	US-10-288-340-6	Sequence 6, Appli
22	18	54.5	6	16	US-10-722-733-6	Sequence 6, Appli
23	18	54.5	6	16	US-10-723-099-6	Sequence 6, Appli
24	18	54.5	6	16	US-10-803-622-197	Sequence 197, App
25	18	54.5	6	16	US-10-803-653-197	Sequence 197, App
26	18	54.5	7	9	US-09-772-105-23	Sequence 23, Appli
27	18	54.5	7	9	US-09-876-388-7	Sequence 7, Appli
28	18	54.5	7	14	US-10-287-892-7	Sequence 7, Appli
29	18	54.5	7	14	US-10-288-340-7	Sequence 7, Appli
30	18	54.5	7	16	US-10-722-733-7	Sequence 7, Appli
31	18	54.5	7	16	US-10-723-099-7	Sequence 7, Appli
32	17	51.5	6	9	US-09-727-963A-38	Sequence 38, Appli
33	17	51.5	6	14	US-10-006-869-636	Sequence 636, App
34	17	51.5	6	14	US-10-006-869-650	Sequence 650, App
35	17	51.5	6	14	US-10-020-354-101	Sequence 101, App
36	17	51.5	6	14	US-10-395-032-636	Sequence 636, App
37	17	51.5	6	14	US-10-395-032-650	Sequence 650, App
38	17	51.5	6	15	US-10-328-953-42	Sequence 42, Appli
39	17	51.5	6	15	US-10-367-580-312	Sequence 312, App
40	17	51.5	6	15	US-10-367-593-312	Sequence 312, App
41	17	51.5	6	15	US-10-367-594-312	Sequence 312, App
42	17	51.5	6	15	US-10-367-654-312	Sequence 312, App
43	17	51.5	6	15	US-10-367-658-312	Sequence 312, App
44	17	51.5	6	15	US-10-367-668-312	Sequence 312, App
45	17	51.5	6	16	US-10-367-674-312	Sequence 312, App

ALIGNMENTS

RESULT 1
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match 72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
: : : : :
Db 1 YTFELSR 7

RESULT 2
US-09-998-909-7
; Sequence 7, Application US/0998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John

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; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: MTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/250,284
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-7

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Query Match          72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 1 YTFELSR 7

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RESULT 3
US-09-826-290-205
; Sequence 205, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-205

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Query Match          72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 FTLEISR 7
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RESULT 4
US-09-826-290-370
; Sequence 370, Application US/09826290
; Patent No. US20020164668A1

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; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-370

Query Match          72.7%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
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RESULT 5
US-09-791-393-145
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; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-145

Query Match          72.7%; Score 24; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 FTLEISR 7
: ||: ||
Db 1 YTFELSR 7

RESULT 6

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 00030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145

Query Match 72.7%; Score 24; DB 10; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
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Db 1 YTFELSR 7

RESULT 7

US-09-791-377-198
; Sequence 198, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-198

Query Match 72.7%; Score 24; DB 11; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
: ||: ||
Db 1 YTFELSR 7

RESULT 8

US-10-264-309-131
; Sequence 131, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 131
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131

Query Match 72.7%; Score 24; DB 15; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7
: ||: ||
Db 1 FTFEYSR 7

RESULT 9

US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 460

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-264-309-460

Query Match 72.7%; Score 24; DB 15; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 1 YTFELSR 7

RESULT 10

US-10-601-100-105

; Sequence 105, Application US/10601100

; Publication No. US20040072261A1

; GENERAL INFORMATION:

; APPLICANT: INNOGENETICS N.V.

; TITLE OF INVENTION: Method for the diagnosis and Differential Diagnosis of

; FILE OF INVENTION: Neurological Diseases

; FILE REFERENCE: 11362.0038.NPUS01

; CURRENT APPLICATION NUMBER: US/10/601,100

; CURRENT FILING DATE: 2003-06-20

; PRIOR APPLICATION NUMBER: EP 02447121.1

; PRIOR FILING DATE: 2002-06-21

; PRIOR APPLICATION NUMBER: US 60/396,437

; PRIOR FILING DATE: 2002-07-17

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 105

; LENGTH: 7

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-601-100-105

Query Match 72.7%; Score 24; DB 15; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 1 YTFELSR 7

RESULT 11

US-10-700-340-52

; Sequence 52, Application US/10700340

; Publication No. US20040203023A1

; GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri

; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST

; FILE OF INVENTION: CANCER

; FILE REFERENCE: 2543-1-032

; CURRENT APPLICATION NUMBER: US/10/700,340

; CURRENT FILING DATE: 2003-11-03

; PRIOR APPLICATION NUMBER: PCT/GB02/02022

; PRIOR FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: GB0110790.3

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: GB0118385.4

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: GB0119791.2

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: GB0120045.0

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: GB0128062.7

; PRIOR FILING DATE: 2001-11-22

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 52

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-700-340-52

Query Match 72.7%; Score 24; DB 17; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.2e+06;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 1 FTFEYSR 7

RESULT 12

US-10-700-340-154

; Sequence 154, Application US/10700340

; Publication No. US20040203023A1

; GENERAL INFORMATION:

; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri

; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BREAST

; FILE OF INVENTION: CANCER

; FILE REFERENCE: 2543-1-032

; CURRENT APPLICATION NUMBER: US/10/700,340

; CURRENT FILING DATE: 2003-11-03

; PRIOR APPLICATION NUMBER: PCT/GB02/02022

; PRIOR FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: GB0110790.3

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: GB0118385.4

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: GB0119791.2

; PRIOR FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: GB0120045.0

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: GB0128062.7

; PRIOR FILING DATE: 2001-11-22

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 154

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-700-340-154

Query Match 72.7%; Score 24; DB 17; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 1 YTFELSR 7

RESULT 13

US-10-050-552A-4

; Sequence 4, Application US/10050552A

; Publication No. US20020187512A1

; GENERAL INFORMATION:

; APPLICANT: Nagem, Ronaldo A.P.

; APPLICANT: Colau, Didier

; APPLICANT: Renaud, Jean-Christophe

; APPLICANT: Dumoutier, Laure

; APPLICANT: Polikarpov, Igor

; TITLE OF INVENTION: Crystal Structure of Interleukin-22

; FILE REFERENCE: LUD-5722 US

; CURRENT APPLICATION NUMBER: US/10/050,552A

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: 60/317,937

; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/333,150

; PRIOR FILING DATE: 2001-11-27

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10
US-10-050-552A-4

Query Match          60.6%; Score 20; DB 13; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLE 4
   ||||
Db 1 FILE 4

RESULT 14
US-10-234-026-6
; Sequence 6, Application US/10234026
; Publication No. US20030097679A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLS.001C1
; CURRENT APPLICATION NUMBER: US/10/234,026
; CURRENT FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: PCT/EP98/02830
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 09/423,468
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Brassica oleracea
US-10-234-026-6

Query Match          60.6%; Score 20; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLEISR 7
   |.:|.
Db 2 TIELSK 7

RESULT 15
US-10-238-965-4
; Sequence 4, Application US/10238965
; Publication No. US20040002586A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Dumoutier, Laure
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/238,965
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/333,150
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; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10
US-10-238-965-4

Query Match          60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLE 4
   ||||
Db 1 FILE 4

Search completed: November 4, 2004, 01:43:17
Job time : 70.6667 secs
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 Seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	100	4	US-09-840-459-32
2	33	100.0	100	4	US-09-497-625A-32
3	33	100.0	112	4	US-09-840-459-55
4	33	100.0	112	4	US-09-497-625A-55
5	33	100.0	113	2	US-08-672-345C-5
6	33	100.0	113	2	US-08-672-345C-6
7	33	100.0	113	2	US-08-672-345C-7
8	33	100.0	113	2	US-08-672-345C-8
9	33	100.0	113	2	US-08-672-345C-95
10	33	100.0	113	2	US-08-672-345C-96
11	33	100.0	113	2	US-08-672-345C-97
12	33	100.0	113	2	US-08-672-345C-98
13	33	100.0	113	3	US-09-214-095D-5
14	33	100.0	113	3	US-09-214-095D-6
15	33	100.0	113	3	US-09-214-095D-7
16	33	100.0	113	3	US-09-214-095D-8
17	33	100.0	113	3	US-09-214-095D-100
18	33	100.0	113	3	US-09-214-095D-104
19	33	100.0	113	3	US-09-214-095D-108
20	33	100.0	113	3	US-09-214-095D-112
21	33	100.0	280	3	US-09-214-095D-119
22	33	100.0	348	4	US-09-646-028-12
23	33	100.0	361	4	US-09-646-028-14
24	30	90.9	192	4	US-09-328-352-5032
25	29	87.9	32	1	US-08-477-877B-33
26	29	87.9	32	1	US-07-977-696C-71
27	29	87.9	32	1	US-08-129-930B-71

28 29 87.9 32 2 US-08-472-281A-33 Sequence 33, Appl
29 29 87.9 32 2 US-08-477-989B-33 Sequence 33, Appl
30 29 87.9 32 3 US-08-976-288A-71 Sequence 71, Appl
31 29 87.9 32 4 US-09-563-222C-80 Sequence 80, Appl
32 29 87.9 32 4 US-09-563-222C-114 Sequence 114, Appl
33 29 87.9 81 1 US-08-497-312-19 Sequence 19, Appl
34 29 87.9 81 4 US-09-254-180C-154 Sequence 154, Appl
35 29 87.9 81 4 US-09-254-180C-155 Sequence 155, Appl
36 29 87.9 81 4 US-09-254-180C-156 Sequence 156, Appl
37 29 87.9 81 4 US-09-254-180C-157 Sequence 157, Appl
38 29 87.9 81 4 US-09-254-180C-158 Sequence 158, Appl
39 29 87.9 81 4 US-09-254-180C-159 Sequence 159, Appl
40 29 87.9 100 4 US-09-472-087-113 Sequence 113, Appl
41 29 87.9 100 4 US-09-472-087-115 Sequence 115, Appl
42 29 87.9 100 4 US-09-840-459-21 Sequence 21, Appl
43 29 87.9 100 4 US-09-840-459-22 Sequence 22, Appl
44 29 87.9 100 4 US-09-840-459-23 Sequence 23, Appl
45 29 87.9 100 4 US-09-840-459-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 33; DB 4; Length 100;
Best local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 2
US-09-497-625A-32
; Sequence 32, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran

; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-32

Query Match 100.0%; Score 33; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 3
US-09-840-459-55
; Sequence 55, Application US/09840459
; Patent No. 6936550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-55

Query Match 100.0%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 4
US-09-497-625A-55
; Sequence 55, Application US/09497625A
; Patent No. 6727349

; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-55

Query Match 100.0%; Score 33; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 5
US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-5

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 6

US-08-672-345C-6
 ; Sequence 6, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 6:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-6

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/672,345C
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/51400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-672-345C-6

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 7

US-08-672-345C-7
 ; Sequence 7, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-7

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 8

US-08-672-345C-8
 ; Sequence 8, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-8

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/672,345C
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 0575/51400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-672-345C-7

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 8

US-08-672-345C-8
 ; Sequence 8, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
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 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
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 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
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 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-7

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 8

US-08-672-345C-8
 ; Sequence 8, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
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 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-8

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 8

US-08-672-345C-8
 ; Sequence 8, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
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 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-8

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 Db 76 FTLEISR 82

RESULT 8

US-08-672-345C-8
 ; Sequence 8, Application US/08672345C
 ; Patent No. 5948658
 ; GENERAL INFORMATION:
 ; APPLICANT: Landry Donald, W.
 ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
 ; NUMBER OF SEQUENCES: 108
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper and Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/672,345C
 ; FILING DATE: 24-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/51400
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-278-0400
 ; TELEFAX: 212-391-0525
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-672-345C-8

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 9
US-08-672-345C-95
; Sequence 95, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-96

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 11
US-08-672-345C-97
; Sequence 97, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-95

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 10
US-08-672-345C-96
; Sequence 96, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA

US-08-672-345C-97

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 12

US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-98

Query Match 100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 13

US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5

; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-5

Query Match 100.0%; Score 33; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14

US-09-214-095D-6
; Sequence 6, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-6

Query Match 100.0%; Score 33; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 15

US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-7

Query Match 100.0%; Score 33; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

Search completed: November 4, 2004, 00:54:52
Job time : 17.6667 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:01:24 ; Search time 37 Seconds
(without alignments)
12.547 Million cell updates/sec

Title: US-09-712-819D-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	60.6	7	1	US-08-222-619-8
2	20	60.6	7	5	PCT-US95-04075-8
3	19	57.6	6	6	5252328-8
4	18	54.5	7	1	US-08-346-333-24
5	18	54.5	7	1	US-09-268-992-78
6	18	54.5	7	3	US-09-657-474-78
7	18	54.5	7	4	US-08-753-750B-20
8	18	54.5	7	5	PCT-US91-07506-24
9	17	51.5	7	2	US-09-174-060-17
10	17	51.5	7	3	US-08-654-623-69
11	17	51.5	7	4	US-08-338-382-17
12	17	51.5	7	4	US-09-345-264-17
13	16	48.5	5	3	US-08-591-632-23
14	16	48.5	5	3	US-09-611-451-23
15	16	48.5	6	1	US-07-717-331F-5
16	16	48.5	6	4	US-08-757-425B-44
17	16	48.5	7	1	US-07-634-641-12
18	16	48.5	7	1	US-08-136-743B-55
19	16	48.5	7	3	US-09-040-216-28
20	16	48.5	7	3	US-09-173-941-72
21	16	48.5	7	4	US-09-423-468A-6
22	16	48.5	7	4	US-09-756-223A-26
23	16	48.5	7	4	US-09-494-190-72
24	15	45.5	4	1	US-08-305-871A-17
25	15	45.5	4	4	US-08-788-822A-1
26	15	45.5	4	4	US-08-134-231C-36
27	15	45.5	4	4	US-08-728-160-36

28	15	45.5	5	1	US-08-136-743B-63	Sequence 63, Appl
29	15	45.5	5	3	US-09-040-216-55	Sequence 55, Appl
30	15	45.5	5	3	US-08-591-632-17	Sequence 17, Appl
31	15	45.5	5	3	US-08-591-632-26	Sequence 26, Appl
32	15	45.5	5	3	US-09-611-451-17	Sequence 17, Appl
33	15	45.5	5	3	US-09-611-451-26	Sequence 26, Appl
34	15	45.5	6	1	US-08-136-743B-62	Sequence 62, Appl
35	15	45.5	6	1	US-08-357-264-6	Sequence 6, Appl
36	15	45.5	6	1	US-08-297-731-4	Sequence 4, Appl
37	15	45.5	6	1	US-08-222-619-21	Sequence 21, Appl
38	15	45.5	6	1	US-08-290-448A-41	Sequence 41, Appl
39	15	45.5	6	1	US-08-672-514-6	Sequence 6, Appl
40	15	45.5	6	1	US-08-290-448A-41	Sequence 41, Appl
41	15	45.5	6	1	US-08-175-069A-41	Sequence 41, Appl
42	15	45.5	6	2	US-08-637-759B-219	Sequence 219, App
43	15	45.5	6	3	US-08-871-355A-219	Sequence 219, App
44	15	45.5	6	3	US-09-040-216-54	Sequence 54, Appl
45	15	45.5	6	3	US-09-623-618B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-222-619-8
; Sequence 8, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Center, Patent Operations/RRR
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-222-619-8

Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7
||| : ||
Db 1 FTPEYSR 7

RESULT 2
PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:

RESULT 4
US-08-346-333-24
; Sequence 24, Application US/08346333
; Patent No. 5677153
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Palzkill, Timothy
; TITLE OF INVENTION: Methods for
; TITLE OF INVENTION: detecting ef

RESULT 5
US-09-268-992-78
; Sequence 78, Application US/09268992
; Patent No. 6342351
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/268,992
; CURRENT FILING DATE: 1999-03-16
; EARLIER APPLICATION NUMBER: 09/236,134
; EARLIER FILING DATE: 1999-01-22
; EARLIER APPLICATION NUMBER: 60/106,056
; EARLIER FILING DATE: 1998-10-28
; EARLIER APPLICATION NUMBER: 60/088,312
; EARLIER FILING DATE: 1998-06-05
; EARLIER APPLICATION NUMBER: 60/078,044
; EARLIER FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-09-268-992-78

Query Match      54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
   :|:|
Db 2 YTMKYS 7

RESULT 6
US-09-657-474-78
; Sequence 78, Application US/09657474
; Patent No. 6399762
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/09/657,474
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-657-474-78

Query Match      54.5%; Score 18; DB 3; Length 7;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKIS 6
   :|:|
Db 2 YTMKYS 7

RESULT 7
US-08-753-750B-20
; Sequence 20, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; FILE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Escherichia coli
US-08-753-750B-20

Query Match      54.5%; Score 18; DB 4; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKI 5
   :|:|
Db 1 FTLSV 5

RESULT 8
PCT-US91-07506-24
; Sequence 24, Application PC/TUS9107506
; GENERAL INFORMATION:
; APPLICANT: Botstein, David
; APPLICANT: Palzkill, Timothy
; TITLE OF INVENTION: Methods for modifying DNA and for
; FILE OF INVENTION: detecting effects of such modification on interaction of
; TITLE OF INVENTION: encoded modified polypeptides with target substrates.
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07506
; FILING DATE: 19911021
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: EP-53469-PC/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-07506-24

Query Match      54.5%; Score 18; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLKI 5
   :|:|
Db 2 TLKI 5

RESULT 9
US-09-174-060-17
; Sequence 17, Application US/09174060
; Patent No. 5989554
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
```

RESULT 10
US-08-654-623-69
; Sequence 69, Application US/08654623
; Patent No. 6010884
; GENERAL INFORMATION:
; APPLICANT: Griffiths, Andrew D
; APPLICANT: Holliger, Kaspar-Philipp
; APPLICANT: Nissim, Ahuva
; APPLICANT: Fisch, Igor
; APPLICANT: Winter, Gregory P
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/654.623

RESULT 11
US-08-338-382-17
; Sequence 17, Application US/08338382
; Patent No. 6069230
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Shultz, John W
; APPLICANT: Lesley, Scott A
; APPLICANT: Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/338,382
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sara, Charles S
;; REGISTRATION NUMBER: 30,492
;; REFERENCE/DOCKET NUMBER: 34506.024
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 608-257-5353
;; TELEFAX: 608-257-9175
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-338-382-17

Query Match 51.5%; Score 17; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
:||||
Db 1 YTLK 4

RESULT 12
US-09-345-264-17
; Sequence 17, Application US/09345264
; Patent No. 6764889
; GENERAL INFORMATION:
; APPLICANT: Knuth, Mark W
; Haak-Frendscho, Mary
; Shultz, John W
; Lesley, Scott A
; Villars, Catherine E
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
; PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
; IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ross & Stevens, S.C.
; STREET: 1 South Pinckney St.
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/345,264
; FILING DATE: 30-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/174,060
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 34506.024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-5353
; TELEFAX: 608-257-9175

;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-345-264-17

Query Match 51.5%; Score 17; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLK 4
:||||
Db 1 YTLK 4

RESULT 13
US-08-591-632-23
; Sequence 23, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-23

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Query Match      48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLK 4
      ||||
Db      2 FTLQ 5

RESULT 14
US-09-611-451-23
; Sequence 23, Application US/09611451
; Patent No. 6395275
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
;           Burton, Dennis R.
;           Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
;                   ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSER: The Scripps Research Institute, Office of
;           Patent Counsel
; STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,451
; FILING DATE: 06-Jul-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/591,632
; FILING DATE: 2001-10-29
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-611-451-23

Query Match      48.5%; Score 16; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLK 4
      ||||
Db      2 FTLQ 5

RESULT 15
US-07-717-331F-5
; Sequence 5, Application US/07717331F
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:36:19 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	74	2	G30538
2	33	100.0	112	1	KVMS16
3	33	100.0	113	1	KVMS1
4	33	100.0	120	1	KVMS67
5	33	100.0	127	2	S40323
6	33	100.0	133	2	S40324
7	29	87.9	54	2	S34093
8	29	87.9	56	2	I5399
9	29	87.9	71	2	H30538
10	29	87.9	72	2	S40358
11	29	87.9	75	2	S40337
12	29	87.9	83	2	S24211
13	29	87.9	83	2	S34095
14	29	87.9	87	2	S34091
15	29	87.9	87	2	S34094
16	29	87.9	89	2	B25155
17	29	87.9	91	2	S24186
18	29	87.9	91	2	S25461
19	29	87.9	93	2	PH1039
20	29	87.9	94	2	PL0258
21	29	87.9	95	2	S40320
22	29	87.9	99	2	E28833
23	29	87.9	99	2	S24504
24	29	87.9	99	2	S24501
25	29	87.9	100	2	S45440
26	29	87.9	100	2	S24681
27	29	87.9	100	2	S26334
28	29	87.9	101	2	C34153
29	29	87.9	101	2	A33730

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30 29 87.9 101 2 PH1057 Ig kappa chain V r
31 29 87.9 102 2 S14590 Ig kappa chain V r
32 29 87.9 102 2 S14591 Ig kappa chain V r
33 29 87.9 102 2 S14594 Ig kappa chain V r
34 29 87.9 102 2 S14592 Ig kappa chain V r
35 29 87.9 102 2 S14593 Ig kappa chain V r
36 29 87.9 102 2 PH1035 Ig light chain V r
37 29 87.9 102 2 E28195 Ig kappa chain V r
38 29 87.9 102 2 PH1044 Ig light chain V r
39 29 87.9 103 2 PH1099 Ig light chain V r
40 29 87.9 103 2 PH1056 Ig light chain V r
41 29 87.9 103 2 PH1100 Ig light chain V r
42 29 87.9 103 2 PH1041 Ig light chain V r
43 29 87.9 103 2 PH1098 Ig light chain V r
44 29 87.9 103 2 PH1040 Ig light chain V r
45 29 87.9 103 2 PH1045 Ig light chain V r
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ALIGNMENTS

RESULT 1

G30538

Ig kappa chain V region (253.15E2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996

C:Accession: G30538

R:Clarlin, J.L.; Berry, J.

J. Immunol. 141, 4012-4019, 1988

A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pne

A:Reference number: A30534; MUID:89035545; PMID:3141511

A:Accession: G30538

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A:Molecule type: mRNA

A:Residues: 1-74 <CLA>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 100.0%; Score 33; DB 2; Length 74;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7

Db 45 FTLEISR 51

RESULT 2

KVMS16

Ig kappa chain V region (M167) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004

C:Accession: A01908

R:Rudikoff, S.; Potter, M.

Biochemistry 17, 2703-2707, 1978

A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot

A:Reference number: A01908; MUID:79000273; PMID:99160

A:Accession: A01908

A:Molecule type: protein

A:Residues: 1-112 <RUD>

A:Cross-references: UNIPROT:P01626

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 14

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 100.0%; Score 33; DB 1; Length 112;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 FTLEISR 7
Db      76 FTLEISR 82

RESULT 3
KWS51
Ig kappa chain V region (M511) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
C:Accession: A01910
R:Appella, E.
Mol. Immunol. 17, 711-718, 1980
A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine
A:Reference number: A01910; MUID:81052016; PMID:6776396
A:Accession: A01910
A:Molecule type: protein
A:Residues: 1-113 <APP>
A:Cross-references: UNIPROT:P01628
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match      100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 FTLEISR 7
Db      76 FTLEISR 82

RESULT 4
KWS57
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A01909
R:Selsing, E.; Storb, U.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:82002223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A:Cross-references: UNIPROT:P01627
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match      100.0%; Score 33; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 FTLEISR 7
Db      96 FTLEISR 102

RESULT 5
S40323
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40323
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40323
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-127 <KLE>
A:Cross-references: EMBL:X72433; NID:G441334; PIDN:CAA51101.1; PID:G441335
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-110/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 33; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 FTLEISR 7
Db      91 FTLEISR 97

RESULT 6
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40324
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: UNIPROT:Q87CD0; EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 33; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 FTLEISR 7
Db      93 FTLEISR 99

RESULT 7
S34093
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 07-May-1999
C:Accession: S34093
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34093
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-54 <WAG>
A:Cross-references: EMBL:X67177
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```

Query Match 87.9%; Score 29; DB 2; Length 54;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 43 FTLKISR 49

RESULT 8
S40358
Ig kappa chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I55399
R:Wuytack, F.; Papp, B.; Verboomen, H.; Raeymaekers, L.; Dode, L.; Bobe, R.; Enouf, J.;
J. Biol. Chem. 269, 1410-1416, 1994
A:Title: A sarco/endoplasmic reticulum Ca(2+)-ATPase 3-type Ca2+ pump is expressed in pl
A:Reference number: I55399; MUID:194117459; PMID:8288608
A:Accession: I55399
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-56 <RES>
A:Cross-references: UNIPROT:Q93084; GB:S68239; NID:G544921; PIDN:AAB29700.1; PID:G544922
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: ATP

Query Match 87.9%; Score 29; DB 2; Length 56;
Best Local Similarity 85.7%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 30 FTLEISR 36

RESULT 9
H30538
Ig kappa chain V region (174.3F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 09-May-1997
C:Accession: H30538
R:Clafalin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Accession: H30538
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-71 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 87.9%; Score 29; DB 2; Length 71;
Best Local Similarity 85.7%; Pred. No. 6.3;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 35 FTLKISR 41

RESULT 10
S40358
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40358
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40358

A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <KDE>
A:Cross-references: EMBL:X72468; NID:G441404; PIDN:CAA51136.1; PID:G441405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 87.9%; Score 29; DB 2; Length 72;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 28 FTLKISR 34

RESULT 11
S40337
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40337
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40337
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-75 <KLE>
A:Cross-references: EMBL:X72447; NID:G441362; PIDN:CAA51115.1; PID:G441363
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 87.9%; Score 29; DB 2; Length 75;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 30 FTLKISR 36

RESULT 12
S24211
Ig kappa chain V region (V3a) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24211
R:Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O reg
A:Reference number: S24205; MUID:91330953; PMID:1907917
A:Accession: S24211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <PAR>
A:Cross-references: EMBL:X59317; NID:G33270; PIDN:CAA42004.1; PID:G33271
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 87.9%; Score 29; DB 2; Length 83;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:||||
Db 59 FTLKISR 65

RESULT 13
S34095
Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34095

R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: UNIPROT:Q8TCD0; UNIPROT:Q9UL80; EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-80/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 83;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:|
Db 61 FTLKISR 67

RESULT 14

S34091
IG kappa chain V region (patient 19 and 20) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S34091; S34092
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34091
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X67175
A:Experimental source: patient 19
A:Accession: S34092
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: EMBL:X67176
A:Experimental source: patient 20
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;3-82/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 87;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:|
Db 63 FTLKISR 69

RESULT 15

S34094
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34094
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34094
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPROT:Q9UL80; EMBL:X67178

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;3-82/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 29; DB 2; Length 87;
Best Local Similarity 85.7%; Pred. No. 7.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
|||:|
Db 63 FTLKISR 69

Search completed: November 4, 2004, 00:48:41
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:41:09 ; Search time 103 Seconds
(without alignments)
39.103 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	112	1 KV2A_MOUSE	P01626 mus musculus
2	33	100.0	113	1 KV2C_MOUSE	P01628 mus musculus
3	33	100.0	120	1 KV2E_MOUSE	P01627 mus musculus
4	30	90.9	306	2 Q87X30	Q87X30 pseudomonas
5	30	90.9	330	2 Q88PD2	Q88PD2 pseudomonas
6	30	90.9	355	2 Q9HE63	Q9HE63 neurospora
7	30	90.9	375	2 Q847Y6	Q847Y6 bacillus pu
8	29	87.9	86	2 Q7Z3Y5	Q7Z3Y5 homo sapien
9	29	87.9	102	2 AAR11040	Aar11040 mus muscu
10	29	87.9	104	2 Q9JL82	Q9JL82 mus musculus
11	29	87.9	104	2 AAR11024	Aar11024 mus muscu
12	29	87.9	104	2 AAR11056	Aar11056 mus muscu
13	29	87.9	105	2 AAR11063	Aar11063 mus muscu
14	29	87.9	105	2 AAR11074	Aar11074 mus muscu
15	29	87.9	109	2 AAR10990	Aar10990 mus muscu
16	29	87.9	112	1 KV2C_HUMAN	P01616 homo sapien
17	29	87.9	113	1 KV2D_HUMAN	P01617 homo sapien
18	29	87.9	113	1 KV2G_MOUSE	P01631 mus musculus
19	29	87.9	114	2 Q9UL80	Q9UL80 homo sapien
20	29	87.9	114	2 AAR11017	Aar11017 mus muscu
21	29	87.9	115	1 KV2A_HUMAN	P01614 homo sapien
22	29	87.9	117	1 KV2E_HUMAN	P06309 homo sapien
23	29	87.9	131	2 Q91234	Q91234 opsanus tau
24	29	87.9	131	2 Q91538	Q91538 xiphias gla
25	29	87.9	133	1 KV2F_HUMAN	P06310 homo sapien
26	29	87.9	148	2 Q8K122	Q8K122 mus musculus
27	29	87.9	238	2 Q99M37	Q99M37 mus musculus
28	29	87.9	238	2 Q8VC16	Q8VC16 mus musculus
29	29	87.9	239	2 Q6P491	Q6P491 homo sapien
30	29	87.9	239	2 Q8K0F8	Q8K0F8 mus musculus
31	29	87.9	239	2 Q8VC55	Q8VC55 mus musculus

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32 29 87.9 239 2 AAH63599 Aah63599 homo sapi
33 29 87.9 240 2 Q6PIH6 Q6pih6 homo sapien
34 29 87.9 240 2 AAH34142 Aah34142 homo sapi
35 29 87.9 502 2 O54994 O54994 mus musculus
36 29 87.9 574 2 Q6DCS6 Q6dcs6 xenopus lae
37 29 87.9 688 1 EFG_APPPP Q9zeu4 apple proli
38 29 87.9 688 2 Q6YQV9 Q6yqv9 onion yello
39 29 87.9 688 2 BAD04349 Bad04349 onion yel
40 29 87.9 760 2 Q7S186 Q7s186 neurospora
41 29 87.9 844 2 Q8N3X5 Q8n3x5 homo sapien
42 29 87.9 869 2 Q71UZ2 Q71uz2 rattus norv
43 29 87.9 869 2 AAC19167 Aac19167 rattus no
44 29 87.9 927 2 Q8C213 Q8c213 mus musculus
45 29 87.9 969 2 Q7PPAS Q7ppas anopheles g

```

ALIGNMENTS

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RESULT 1
KV2A_MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
RL Biochemistry 17:2703-2707(1978).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine. The sequence of the V region of the heavy
CC chain has also been determined.
DR PIR; A01908; KVAS16.
DR HSSP; Q8K0F8; 1KN2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 33; DB 1; Length 112;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FTLEISR 7
Db 76 FTLEISR 82

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RESULT 2
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;

```

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC binds phosphorylcholine.
DR PIR; A01910; KVMSS1.
DR HSSP; Q8K0F8; 1KX2.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLEISR 7
DB 76 FTLEISR 82

RESULT 3
KV2B MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region VKappa167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832;
RA Selsing B., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
RT genes.";
RL Cell 25:47-58(1981).
CC -----
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DR EMBL; J00562; AAA39032.1; -.
DR EMBL; K02415; AAA39051.1; -.
DR PIR; A01909; KVMSS7.
DR HSSP; P01751; INOB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120 Ig kappa chain V-II region VKappa167.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 120 Complementarity-determining-3.
FT DISULFID 43 113 By similarity.
SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

Query Match 100.0%; Score 33; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 8.3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLEISR 7
DB 96 FTLEISR 102

RESULT 4
O87X30 PRELIMINARY; PRT; 306 AA.
AC Q87X30;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Dehydrogenase, putative.
GN OrderedLocusNames-PSPT04360;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Daviden T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AB016871; AAC57810.1; -.
DR TIGR; PSPT04360; -.
KW Complete proteome.
SQ SEQUENCE 306 AA; 34515 MW; D13FCA5790ACB33D CRC64;

Query Match 90.9%; Score 30; DB 2; Length 306;
Best Local Similarity 85.7%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0;

QY 1 FTLEISR 7
DB 270 FTLEISR 276
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RESULT 5
Q88PD2
AC Q88PD2; PRELIMINARY; PRT; 330 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 3-beta hydroxysteroid dehydrogenase/isomerase family protein,
DE putative.
DE OrderedLocusNames=PP0918;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzez A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016777; AAN66543.1; -.
DR TIGR; PP0918; -.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR Complete proteome; Isomerase.
SQ SEQUENCE 330 AA; 37056 MW; A60498B263D91AC5 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 330;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 294 FTLEISR 300
[1]

RESULT 6
Q9HE63
ID Q9HE63 PRELIMINARY; PRT; 355 AA.
AC Q9HE63;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Related to cyclin homolog UME3.
GN Name=B2108.140;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RX Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AL451012; CAC18151.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin-like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.

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KW Cyclin.
SQ SEQUENCE 355 AA; 39661 MW; A081A8CC97B9B00E CRC64;

Query Match 90.9%; Score 30; DB 2; Length 355;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 61 FTLEISR 67
[1]

RESULT 7
Q847Y6 PRELIMINARY; PRT; 375 AA.
ID Q847Y6;
AC Q847Y6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gyrase B subunit (Fragment).
GN Name=gyrB;
OS Bacillus pumilus (Bacillus mesentericus).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1408;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FO-036D;
RA Chen F., Venkateswaran K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA gyrase negatively supercoils closed circular double-
CC stranded DNA in an ATP-dependent manner and also catalyzes the
CC interconversion of other topological isomers of double-stranded
CC DNA rings, including catenanes and knotted rings (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.
DR EMBL; AY167867; AAO61450.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR001241; DNA topoisom.
DR Pfam; PF00204; DNA gyraseB; 1.
DR PRINTS; PR00418; TP12FAMILY.
DR SMART; SM00433; TOP2c; 1.
DR PROSITE; PS00177; TOPOISOMERASE II; 1.
KW ATP-binding; Isomerase; Topoisomerase.
FT NON_TER 1
FT NON_TER 375
SQ SEQUENCE 375 AA; 41568 MW; 04A49AD8704E3A6D CRC64;

Query Match 90.9%; Score 30; DB 2; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 364 FTLEISR 370
[1]

RESULT 8
Q7Z3Y5 PRELIMINARY; PRT; 86 AA.
ID Q7Z3Y5;
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKA17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hodgkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Braunniger A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564426; CAD92033.1; -.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 86
FT NON_TER 86
SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match      87.9%; Score 29; DB 2; Length 86;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 55 FTLKISR 61

RESULT 9
AAR11040 ID AAR11040 PRELIMINARY; PRT; 102 AA.
AC AAR11040;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RA "Antinuclear autoantibodies from B6.S1el mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436880; AAR11040.1; -.
FT NON_TER 102
FT NON_TER 102
SQ SEQUENCE 102 AA; 11112 MW; A08600D2B09ABA92 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 102;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 74 FTLKISR 80

RESULT 10
Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
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RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "t-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206024; AAF69322.1; -.
DR PIR; S26334; S26334.
DR PDB; 1DLF; X-ray; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 104
FT NON_TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 68 FTLKISR 74

RESULT 11
AAR11024 ID AAR11024 PRELIMINARY; PRT; 104 AA.
AC AAR11024;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RA "Antinuclear autoantibodies from B6.S1el mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436864; AAR11024.1; -.
FT NON_TER 104
FT NON_TER 104
SQ SEQUENCE 104 AA; 11310 MW; 2CF631F3058E2BB9 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 73 FTLKISR 79

RESULT 12
AAR11056 ID AAR11056 PRELIMINARY; PRT; 104 AA.
AC AAR11056;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436896; AAR11056.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11327 MW; BFC116BEF36AB51A CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 73 FTLKISR 79

RESULT 13
AAR11063
ID AAR11063 PRELIMINARY; PRT; 104 AA.
AC AAR11063;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436903; AAR11063.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11304 MW; 9358D08600C5E65A CRC64;

Query Match      87.9%; Score 29; DB 2; Length 104;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 74 FTLKISR 80

RESULT 14
AAR11074
ID AAR11074 PRELIMINARY; PRT; 105 AA.
AC AAR11074;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436914; AAR11074.1; -.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11378 MW; BCB358D08600CEC0 CRC64;
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Query Match      87.9%; Score 29; DB 2; Length 105;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 74 FTLKISR 80

RESULT 15
AAR10990
ID AAR10990 PRELIMINARY; PRT; 109 AA.
AC AAR10990;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436830; AAR10990.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11894 MW; BFA0941FA01908FD CRC64;

Query Match      87.9%; Score 29; DB 2; Length 109;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 68 FTLKISR 74

Search completed: November 4, 2004, 00:53:57
Job time : 105 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 Seconds
(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	33	100.0	32	7 ADM08848	Adm08848 Canine im
2	33	100.0	32	7 ADM08851	Adm08851 Canine im
3	33	100.0	32	7 ADM08547	Adm08547 Canine im
4	33	100.0	32	7 ADM08548	Adm08548 Canine im
5	33	100.0	100	4 AAE06969	Aae06969 Mouse ger
6	33	100.0	104	2 AAR40214	Aar40214 Sequence
7	33	100.0	111	5 ABG76560	Abg76560 HCV EL an
8	33	100.0	112	4 AAE06992	Aae06992 Human kap
9	33	100.0	113	2 AAW39803	Aaw39803 Variable
10	33	100.0	113	2 AAW39886	Aaw39886 Light cha
11	33	100.0	113	2 AAW39802	Aaw39802 Variable
12	33	100.0	113	2 AAW39801	Aaw39801 Variable
13	33	100.0	113	2 AAW39882	Aaw39882 Light cha
14	33	100.0	113	2 AAW39804	Aaw39804 Variable
15	33	100.0	113	8 ADI21215	Adi21215 Anti-plat
16	33	100.0	121	2 AAR47511	Aar47511 LSH241 l
17	33	100.0	122	3 AAY70790	Aay70790 Murine an
18	33	100.0	145	3 AAY32261	Aay32261 Mouse ant
19	33	100.0	178	5 ABP43484	Abp43484 Human sec
20	33	100.0	248	7 ADG32323	Adg32323 Mouse scf
21	33	100.0	274	2 AAW39899	Aaw39899 Single ch
22	33	100.0	317	7 ADG32360	Adg32360 Precursor
23	33	100.0	348	2 AAY29910	Aay29910 Human IP-
24	33	100.0	361	2 AAY29912	Aay29912 Human MCP
25	31	93.9	715	8 ADN38471	Adn38471 Novel hum

26	30	90.9	192	6	ADA33745	Ada33745 Acinetoba
27	30	90.9	330	6	ABU39673	Abu39673 Protein e
28	30	90.9	330	6	ABU41467	Abu41467 Protein e
29	30	90.9	335	6	ABU27800	Abu27800 Protein e
30	29	87.9	32	2	AAW79207	Aaw79207 Framework
31	29	87.9	32	4	AAW86295	Aaw86295 Murine de
32	29	87.9	32	5	ABP62672	Abp62672 Human imm
33	29	87.9	32	5	ABP62674	Abp62674 Human imm
34	29	87.9	32	5	AAU70400	Aau70400 Human lig
35	29	87.9	32	5	AAU70440	Aau70440 Mouse lig
36	29	87.9	32	7	ADM08541	Adm08541 Canine im
37	29	87.9	32	7	ADM08539	Adm08539 Canine im
38	29	87.9	32	8	ADL93640	Adl93640 Human CD4
39	29	87.9	32	8	ADL93554	Adl93554 Human CD4
40	29	87.9	37	8	ADQ31286	Adq31286 Humanised
41	29	87.9	50	5	ABG30477	Abg30477 Human ant
42	29	87.9	50	5	ABG30478	Abg30478 Human ant
43	29	87.9	50	5	ABG30479	Abg30479 Human ant
44	29	87.9	81	2	AAR92994	Aar92994 Homologou
45	29	87.9	89	2	AAR80082	Aar80082 Mouse der

ALIGNMENTS

RESULT 1
ADM08848
ID ADM08848 standard; peptide; 32 AA.
XX
AC ADM08848;
XX
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL species framework 3 peptide 60.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW anti-allergic; allergy; Igb; gene therapy; kappa species; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (IDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
DR WPI; 2003-598521/56.
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Claim 43; Page 111; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC anti-allergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (PR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLISR 7
 DB 15 FTLISR 21

RESULT 2
 ADM08851
 ID ADM08851 standard; peptide; 32 AA.
 XX AC ADM08851;
 XX 20-MAY-2004 (first entry)
 DT
 DE Canine immunoglobulin kappa VL species framework 3 peptide 63.
 XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW antiallergic; allergy; IgE; gene therapy; kappa species; VL framework;
 KW FR3.
 XX Canis familiaris.
 OS WO2003060080-A2.
 XX 24-JUL-2003.
 PD 20-DEC-2002; 2002WO-US041362.
 XX 21-DEC-2001; 2001US-0344874P.
 PF 21-DEC-2001; 2001US-0344874P.
 XX (IDEX-) IDEXX LAB INC.
 PR Krah ER, Guo H, Aiyappa A, Lawton R;
 PI WPI; 2003-598521/56.
 XX New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 PT Claim 43; Page 111; 130pp; English.
 XX The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a canine
 CC immunoglobulin light chain variable domain framework (FR) peptide of the
 CC invention.
 XX Sequence 32 AA;
 SQ Query Match 100.0%; Score 33; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLISR 7
 DB 15 FTLISR 21

RESULT 3
 ADM08547
 ID ADM08547 standard; peptide; 32 AA.
 XX AC ADM08547;
 XX 20-MAY-2004 (first entry)
 DT
 DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 24.
 XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
 KW FR3.
 XX Canis familiaris.
 OS

XX WO2003060080-A2.
 EN 24-JUL-2003.
 PD 20-DEC-2002; 2002WO-US041362.
 XX 21-DEC-2001; 2001US-0344874P.
 PF 21-DEC-2001; 2001US-0344874P.
 XX (IDEX-) IDEXX LAB INC.
 PR Krah ER, Guo H, Aiyappa A, Lawton R;
 PI WPI; 2003-598521/56.
 XX New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 PT Claim 42; Page 109; 130pp; English.
 XX The invention relates to a novel canine heavy or light chain variable
 CC domain polypeptide. The protein of the invention demonstrates
 CC antiallergic activity and may be useful for treating canine allergy,
 CC possibly via gene therapy. The current sequence is that of a canine
 CC immunoglobulin light chain variable domain framework (FR) peptide of the
 CC invention.
 XX Sequence 32 AA;
 SQ Query Match 100.0%; Score 33; DB 7; Length 32;
 Best Local Similarity 100.0%; Pred. No. 4.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLISR 7
 DB 15 FTLISR 21

RESULT 4
 ADM08548
 ID ADM08548 standard; peptide; 32 AA.
 XX AC ADM08548;
 XX 20-MAY-2004 (first entry)
 DT
 DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 25.
 XX canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
 KW antiallergic; allergy; IgE; gene therapy; kappa subgenus; VL framework;
 KW FR3.
 XX Canis familiaris.
 OS WO2003060080-A2.
 XX 24-JUL-2003.
 PD 20-DEC-2002; 2002WO-US041362.
 XX 21-DEC-2001; 2001US-0344874P.
 PF 21-DEC-2001; 2001US-0344874P.
 XX (IDEX-) IDEXX LAB INC.
 PR Krah ER, Guo H, Aiyappa A, Lawton R;
 PI WPI; 2003-598521/56.
 XX New canine heavy and light chain variable domain polypeptides, useful for
 PT treating canine allergy.
 PT Claim 42; Page 109; 130pp; English.
 XX

CC The invention relates to a novel canine heavy or light chain variable domain polypeptide. The protein of the invention demonstrates CC antiallergic activity and may be useful for treating canine allergy, CC possibly via gene therapy. The current sequence is that of a canine CC immunoglobulin light chain variable domain framework (FR) peptide of the CC invention.

XX
CC
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21
|||||

RESULT 5
AAE06969
ID AAE06969 standard; protein; 100 AA.
AC AAE06969;
XX
XX
DT 16-OCT-2001 (first entry)
XX
XX
DE Mouse germline kappa light chain variable (VK) region, 167/24.
XX
XX
KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; VK; kappa light chain variable region.

XX
XX
OS Mus sp.
XX
XX
EN WO200157226-A1.
XX
XX
PD 09-AUG-2001.
XX
XX
PF 02-FEB-2001; 2001WO-US003537.
XX
XX
PR 03-FEB-2000; 2000US-00497625.
XX
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX
XX
DR WPI; 2001-488888/53.
XX
XX
PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-antigen binding region and human immunoglobulin.

XX
XX
PS Disclosure; Page 151; 183pp; English.

XX
XX
CC The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and restenosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute

CC inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24

XX
CC
XX
SQ Sequence 100 AA;
Query Match 100.0%; Score 33; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82
|||||

RESULT 6
AAE02114
ID AAE02114 standard; protein; 104 AA.
XX
XX
AC AAE02114;
XX
XX
DT 25-MAR-2003 (revised)
DT 04-FEB-1994 (first entry)
XX
XX
DE Sequence of mouse hybridoma cell line RF-HBs-1 antibody light chain.

XX
XX
KW Humanised antibody; complementarity determining region; hepatitis B virus; surface antigen.

XX
XX
OS Synthetic.

XX
XX
EN WO9316192-A1.
XX
XX
PD 19-AUG-1993.
XX
XX
PF 09-FEB-1993; 93WO-GB000267.
XX
XX
PR 11-FEB-1992; 92GB-00002796.
XX
XX
PA (WELL) WELLCOME FOUND LTD.
XX
XX
PI Crowe JS;
XX
XX
DR WPI; 1993-272894/34.
XX
XX
PT N-PSDB; AAQ48172.

XX
XX
PT Humanised antibody against hepatitis - has complementarity determining regions of variable domains from a non-human antibody and constant domains from a human antibody.

XX
XX
PS Disclosure; Page 24-25; 48pp; English.

XX
XX
CC A humanised antibody is claimed in which the AA sequences of the CDRs are at least 60% homologous with light chain CDRs 1-3, and heavy chain CDRs 1-3 (see AAQ48174-9, AAR40216-21). The first step to humanise a monoclonal antibody by CDR-grafting is to determine the nucleotide and predicted AA sequence of the starting antibody light and heavy variable domains. The simplest method is from cDNA. RF-HBs-1 is an hybridoma cell line. Its Mabs contain mouse anti-hepatitis B surface antigen heavy and light chains. The nucleotide and predicted AA sequence of the mouse RF-HBs-1 antibody chains are shown in AAQ48172/R40214 (light) and AAQ48173/R40215 (heavy). (Updated on 25-MAR-2003 to correct PN field.)

XX
XX
SQ Sequence 104 AA;
Query Match 100.0%; Score 33; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 |||||

Db 76 FTLEISR 82

RESULT 7
 ABG76560
 ID ABG76560 standard; protein; 111 AA.
 AC ABG76560;
 XX
 DT 05-NOV-2002 (first entry)
 DE HCV E1 antigen monoclonal antibody #48.
 XX Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 XX Homo sapiens.
 OS
 PN WO200260954-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 14-JAN-2002; 2002WO-SE000044.
 XX
 PR 12-JAN-2001; 2001US-0260889P.
 XX
 PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX
 PI Drakenberg K, Persson MAA;
 DR WPI; 2002-608502/65.
 XX
 PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 XX
 PS Disclosure; Page 53; 64pp; English.
 XX
 CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 33; DB 5; Length 111;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 |||||

Db 75 FTLEISR 81

RESULT 8
 AAE06992
 ID AAE06992 standard; protein; 112 AA.
 AC AAE06992;
 XX
 DT 16-OCT-2001 (first entry)
 XX Human kappa light chain variable (VK) region, H66.
 DE Human; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 XX

KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
 KW inflammatory glomerulopathy; vascular intervention; ID9 antibody;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region
 FT 24.39
 FT /label= CDR1
 FT /note= "Complementarity determining region 1"
 FT 55.61
 FT /label= CDR2
 FT /note= "Complementarity determining region 2"
 FT 94.102
 FT /label= CDR3
 FT /note= "Complementarity determining region 3"
 FT
 XX WO200157226-A1.
 PN
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US003537.
 XX
 PR 03-FEB-2000; 2000US-00497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
 DR WPI; 2001-488888/53.
 XX
 PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
 PT disorder in a patient, comprises a binding specificity for CCR2, and a
 PT non-human antigen binding region and human immunoglobulin.
 XX
 PS Disclosure; Page 159-160; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
 CC comprising an antigen binding region of non-human origin and at least a
 CC portion of an immunoglobulin of human origin. The humanised antibodies
 CC are useful for inhibiting the interaction of a cell expressing CCR2. They
 CC are useful for inhibiting or treating HIV infection. The proteins of the
 CC invention are useful for inhibiting leukocyte trafficking, for treating
 CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
 CC disorders such as rheumatoid arthritis and multiple sclerosis,
 CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
 CC are useful in therapy or diagnosis, and in the manufacture of a
 CC medicament for treating CCR-2 mediated disease. They are also useful for
 CC treating allergy, anaphylaxis, malignancy, chronic and acute
 CC inflammation, histamine and IgE mediated allergic reaction, shock,
 CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
 CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
 CC associated with vascular intervention, including angioplasty and/or stent
 CC placement in a mammal. Humanised antibodies are also useful for
 CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
 CC neointimal hyperplasia of a vessel in a mammal, preferably associated
 CC with vascular intervention. The present sequence is human kappa light
 CC chain variable (VK) region, H66
 XX
 SQ Sequence 112 AA;
 Query Match 100.0%; Score 33; DB 4; Length 112;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
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Db      76 FTLEISR 82

RESULT 9
AAW39803
ID      AAW39803 standard; protein; 113 AA.
XX      AC
XX      AAW39803;
XX      DT 16-JUN-1998 (first entry)
XX      DE
XX      DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
XX      KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX      KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX      KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX      KW overdose; addition.
XX      OS
XX      Mus sp.
XX      PN WO9749800-A1.
XX      PD 31-DEC-1997.
XX      PF 25-JUN-1997; 97WO-US010965.
XX      PR 25-JUN-1996; 96US-00672345.
XX      PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX      PI Landry DW;
XX      DR WPI; 1998-077166/07.
XX      DR N-PSDB; AAV09793.
XX      PT
XX      PT New catalytic antibodies able to decompose cocaine, single-chain
XX      PT analogues - used to treat cocaine overdose and addition, required in far
XX      PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX      PS Disclosure; Fig 19; 147pp; English.
XX      CC
XX      CC The present sequence represents the light chain of a catalytic antibody
XX      CC which is capable of degrading cocaine. A series of cocaine transition
XX      CC state analogues (TSAs) were prepared and used to immunise mice for
XX      CC production of hybridomas. Catalytic antibodies were identified by their
XX      CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
XX      CC antibodies reduce the concentration of cocaine in a subject, and are used
XX      CC particularly for the treatment of an overdose. They are also used for
XX      CC treating addiction (by reducing the in vivo concentration that can be
XX      CC achieved)
XX      SQ Sequence 113 AA;

Query Match      100.0%; Score 33; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FTLEISR 7
Db      76 FTLEISR 82

RESULT 11
AAW39802
ID      AAW39802 standard; protein; 113 AA.
XX      AC
XX      AAW39802;
XX      DT 16-JUN-1998 (first entry)
XX      DE
XX      DE Variable domain of the Kappa light chain of catalytic antibody 6A12.
XX      KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX      KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX      KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX      KW overdose; addition.
XX      OS
XX      Mus sp.
XX      PN WO9749800-A1.
XX      PD 31-DEC-1997.
XX      PF 25-JUN-1997; 97WO-US010965.
XX      PT
XX      PT Light chain of the catalytic antibody 6A12.

```

PR 25-JUN-1996; 96US-00672345.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 PA Landry DW;
 PI WPI; 1998-077166/07.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 XX smaller doses than antibodies that antagonise cocaine by simply binding.
 PS Claim 14; Page 72; 147pp; English.
 XX AAW39801-05 represent the amino acid sequences of the variable domain of
 CC the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 6A12 has a per minute Kcat of 0.072. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX Sequence 113 AA;
 Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLEISR 7
 Db 76 FTLEISR 82
 RESULT 12
 AAW39801
 ID AAW39801 standard; protein; 113 AA.
 AC AAW39801;
 XX 16-JUN-1998 (first entry)
 DT Variable domain of the Kappa light chain of catalytic antibody 3B9.
 DE Variable domain; lambda light chain; catalytic antibody; degradation;
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
 XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX overdose; addiction.
 OS Mus sp.
 XX WO9749800-A1.
 EN 31-DEC-1997.
 PD 25-JUN-1997; 97WO-US010965.
 XX 25-JUN-1996; 96US-00672345.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX Landry DW;
 PI WPI; 1998-077166/07.
 DR P-PSDB; AAW09791.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 XX smaller doses than antibodies that antagonise cocaine by simply binding.

XX Claim 12; Page 71-72; 147pp; English.
 PS AAW39801-05 represent the amino acid sequences of the variable domain of
 XX the Kappa light chain of catalytic antibodies which are able to degrade
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release 3H-
 CC benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state analogue.
 CC Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for the
 CC treatment of an overdose. They are also used for treating addiction (by
 CC reducing the in vivo concentration that can be achieved)
 XX Sequence 113 AA;
 Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLEISR 7
 Db 76 FTLEISR 82
 RESULT 13
 AAW39882
 ID AAW39882 standard; protein; 113 AA.
 AC AAW39882;
 XX 16-JUN-1998 (first entry)
 DT Light chain of the catalytic antibody 2A10.
 DE Variable domain; lambda light chain; catalytic antibody; degradation;
 XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
 XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 XX overdose; addiction.
 OS Mus sp.
 XX WO9749800-A1.
 EN 31-DEC-1997.
 PD 25-JUN-1997; 97WO-US010965.
 XX 25-JUN-1996; 96US-00672345.
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX Landry DW;
 PI WPI; 1998-077166/07.
 DR N-PSDB; AAW09789.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required in far
 XX smaller doses than antibodies that antagonise cocaine by simply binding.
 PS Disclosure; Fig 21; 147pp; English.
 XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be

CC achieved)

SQ Sequence 113 AA;

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 |||||
 76 FTLEISR 82

Db

RESULT 14
 AAW39804

ID AAW39804 standard; protein; 113 AA.

XX

AC AAW39804;

XX

DT 16-JUN-1998 (first entry)

XX

DE Variable domain of the Kappa light chain of catalytic antibody 2A10.

XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
 cocaine; cocaine transition state analogue; TSA; benzoic acid;
 phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 overdose; addiction.

KW

XX Mus sp.

OS

XX WO9749800-A1.

XX

XX 31-DEC-1997.

XX

XX 25-JUN-1997; 97WO-US010965.

XX

XX 25-JUN-1996; 96US-00672345.

XX

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX

XX Landry DW;

XX

XX WPI; 1998-077166/07.

XX

XX New catalytic antibodies able to decompose cocaine, single-chain
 analogues - used to treat cocaine overdose and addiction, required in far
 smaller doses than antibodies that antagonise cocaine by simply binding.

XX

XX Claim 16; Page 73-74; 147pp; English.

XX

XX AAW39801-05 represent the amino acid sequences of the variable domain of
 the Kappa light chain of catalytic antibodies which are able to degrade
 cocaine. A series of cocaine transition state analogues (TSAs) were
 prepared and used to immunise mice for production of hybridomas.
 Catalytic antibodies were identified by their capacity to release 3H-
 benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 represents the heavy chain) was identified using TSA1 which is an
 immunogenic conjugate of a phosphate monoester transition state analogue.
 Antibody 2A10 has a per minute Kcat of 0.011. The antibodies reduce the
 concentration of cocaine in a subject, and are used particularly for the
 treatment of an overdose. They are also used for treating addiction (by
 reducing the in vivo concentration that can be achieved)

XX

SQ Sequence 113 AA;

Query Match 100.0%; Score 33; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
 |||||
 76 FTLEISR 82

Db

RESULT 15
 ADI22125

ID ADI22125 standard; protein; 113 AA.

XX

AC ADI22125;

XX

DT 22-APR-2004 (first entry)

XX

DE Anti-platelet autoantibody related light chain amino acid L49 SEQ:88.

XX

KW anti-platelet autoantibody; autoantibody; blood clotting inhibition;
 thrombus; platelet adhesion inhibition;
 thrombotic thrombocytopenic purpura; platelet aggregation inhibition;
 idiopathic thrombocytopenic purpura; haemostatic; anticoagulant;
 thrombolytic; human.

KW

XX Homo sapiens.

OS

XX Synthetic.

XX

XX WO2004005890-A2.

XX

XX 15-JAN-2004.

XX

XX 03-JUL-2003; 2003WO-US021304.

XX

XX 03-JUL-2002; 2002US-0394352P.

XX

XX 18-SEP-2002; 2002US-0411694P.

XX

XX (UYPE-) UNIV PENNSYLVANIA.

XX

XX Siegel DL;

XX

XX WPI; 2004-142998/14.

XX

XX N-PSDB; ADI22072.

XX

XX Claim 12; SEQ ID NO 88; 232pp; English.

XX

XX The present invention describes a method (M1) for identifying an anti-
 platelet autoantibody (I) in a mammal. The autoantibody is detected by
 producing an antibody phage display library from B-lymphocytes obtained
 from the mammal, and screening the library to detect a phage that
 specifically binds with a platelet component, where the screening
 comprises panning the phage on intact platelets using competitive cell-
 surface panning. Also described: (1) an autoantibody identified by (M1);
 (2) an isolated nucleic acid encoding an anti-platelet autoantibody; (3)
 inhibiting (M2) blood clotting in a mammal having a thrombus or at risk
 of thrombus formation; (4) reversibly (M3) inhibiting blood clotting in a
 mammal having a thrombus or at risk of thrombus formation; (5) inhibiting
 (M4) binding of an anti-platelet autoantibody with a platelet component;
 (6) inhibiting (M5) platelet adhesion in a mammal; (7) treating (M6)
 thrombotic thrombocytopenic purpura in a mammal; (8) inhibiting (M7)
 platelet aggregation; (9) inhibiting (M8) platelet activation; (10)
 inhibiting (M9) platelet function; (11) inhibiting (M10) binding of an
 anti-platelet autoantibody, or its biologically active fragment with a
 platelet; (12) identifying (M11) a peptide that inhibits binding of an
 anti-platelet autoantibody with a platelet; (13) a peptide identified by
 the method of (12); (14) a peptide that specifically binds with an anti-
 platelet autoantibody; (15) treating (M12) idiopathic thrombocytopenic
 purpura (ITP) in a mammal; and (16) a kit for reversibly inhibiting blood
 clotting, inhibiting platelet aggregation, inhibiting platelet function
 or inhibiting platelet activation comprising an amount of an anti-
 platelet autoantibody, or its biologically active fragment that
 specifically binds with glycoprotein IIb/IIIa, where the autoantibody, or
 its fragment comprises an antigen binding region derived from an H44L4
 anti-platelet autoantibody, the kit further comprising a peptide
 inhibitor of the binding with glycoprotein IIb/IIIa, and an applicator
 and an instructions for use. (I) has haemostatic, anticoagulant and
 thrombolytic activities. The autoantibodies (I) are useful for diagnosing
 and for developing therapeutics for diseases mediated by autoantibody
 binding with platelet antigens. (M6) and (M12) are useful for treating
 thrombotic thrombocytopenic purpura and idiopathic thrombocytopenic
 purpura, respectively. (M2) and (M3) are useful for inhibiting blood

```

CC clotting. The present sequence is used in the exemplification of the
CC present invention.
XX
SQ Sequence 113 AA;
    Query Match      100.0%; Score 33; DB 8; Length 113;
    Best Local Similarity 100.0%; Pred. No. 15;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 FTLEISR 7
Db      76 FTLEISR 82

Search completed: November 4, 2004, 00:47:41
Job time : 62.3333 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 seconds
(without alignments)
31.376 Million cell updates/sec

Title: US-09-712-819D-12

Perfect score: 33

Sequence: 1 FTLEISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	33	100.0	32	16	US-10-327-598-403
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4	33	100.0	100	16	US-10-766-773-32
5	33	100.0	100	16	US-10-766-610-32
6	33	100.0	100	16	US-10-733-563-32
7	33	100.0	111	17	US-10-466-242-48
8	33	100.0	112	9	US-09-840-459-55
9	33	100.0	112	16	US-10-766-773-55
10	33	100.0	112	16	US-10-766-610-55
11	33	100.0	112	16	US-10-733-563-55
12	33	100.0	113	10	US-09-940-727B-5
13	33	100.0	113	10	US-09-940-727B-6

14	33	100.0	113	10	US-09-940-727B-7	Sequence 7, Appli
15	33	100.0	113	10	US-09-940-727B-8	Sequence 8, Appli
16	33	100.0	113	10	US-09-940-727B-100	Sequence 100, App
17	33	100.0	113	10	US-09-940-727B-104	Sequence 104, App
18	33	100.0	113	10	US-09-940-727B-108	Sequence 108, App
19	33	100.0	113	10	US-09-940-727B-112	Sequence 112, App
20	33	100.0	178	16	US-10-398-037-8	Sequence 8, Appli
21	33	100.0	280	10	US-09-940-727B-119	Sequence 119, App
22	33	100.0	348	14	US-10-335-394-12	Sequence 12, Appl
23	33	100.0	361	14	US-10-335-394-14	Sequence 14, Appl
24	30	90.9	329	14	US-10-369-493-13704	Sequence 13704, A
25	30	90.9	330	15	US-10-282-122A-67597	Sequence 67597, A
26	30	90.9	330	15	US-10-282-122A-69391	Sequence 69391, A
27	30	90.9	335	15	US-10-282-122A-55724	Sequence 55724, A
28	30	90.9	375	14	US-10-369-493-4199	Sequence 4199, Ap
29	29	87.9	32	10	US-09-563-222-80	Sequence 80, Appl
30	29	87.9	32	10	US-09-563-222-120	Sequence 120, App
31	29	87.9	32	10	US-09-947-839-71	Sequence 71, Appl
32	29	87.9	32	14	US-10-168-809-5	Sequence 5, Appli
33	29	87.9	32	16	US-10-663-244-49	Sequence 49, Appl
34	29	87.9	32	16	US-10-663-244-135	Sequence 135, App
35	29	87.9	32	16	US-10-327-598-385	Sequence 385, App
36	29	87.9	32	16	US-10-327-598-389	Sequence 389, App
37	29	87.9	32	17	US-10-783-950-80	Sequence 80, Appl
38	29	87.9	32	17	US-10-783-950-114	Sequence 114, App
39	29	87.9	93	9	US-09-905-243-61	Sequence 61, Appl
40	29	87.9	99	14	US-10-041-860-281	Sequence 281, App
41	29	87.9	99	14	US-10-041-860-323	Sequence 323, App
42	29	87.9	99	14	US-10-041-860-365	Sequence 365, App
43	29	87.9	99	14	US-10-308-817-176	Sequence 176, App
44	29	87.9	99	15	US-10-453-698-176	Sequence 176, App
45	29	87.9	100	9	US-09-822-698A-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-327-598-401
; Sequence 401, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aliyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 401
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-401

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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7

Db 15 FTLEISR 21

RESULT 2

US-10-327-598-403

; Sequence 403, Application US/10327598

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; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 403
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-403

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Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLEISR 7
DB 15 FTLEISR 21

RESULT 3
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 33; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 76 FTLEISR 82

RESULT 4
US-10-766-773-32
; Sequence 32, Application US/10766773
; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-773-32

Query Match 100.0%; Score 33; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 76 FTLEISR 82

RESULT 5
US-10-766-610-32
; Sequence 32, Application US/10766610
; Publication No. US20040132980A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-32

Query Match 100.0%; Score 33; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
DB 76 FTLEISR 82
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 6
US-10-733-563-32
; Sequence 32, Application US/10733563
; Publication No. US20040151721A1
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; CURRENT FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-10-17
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 7
US-10-466-242-48
; Sequence 48, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(111)
; OTHER INFORMATION: Clone 2b:5 VK
US-10-466-242-48

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
Db 76 FTLEISR 82

Db 75 FTLEISR 81

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US-09-840-459-55
; Sequence 55, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-55

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Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
Db 76 FTLEISR 82

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; Publication No. US20040126851A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-766-773-55

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Db	76 FTLEISR 82					
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; Publication No. US20040132980A1						
; GENERAL INFORMATION:						
; APPLICANT: LaRosa, Gregory J.						
; APPLICANT: Horvath, Christopher						
; APPLICANT: Newman, Walter						
; APPLICANT: Jones, S. Tarran						
; APPLICANT: O'Brien, Siobhan H.						
; APPLICANT: O'Keefe, Theresa						
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND						
; FILE REFERENCE: 1855.1052-029						
; CURRENT APPLICATION NUMBER: US/10/766,610						
; CURRENT FILING DATE: 2004-01-27						
; PRIOR APPLICATION NUMBER: 09/840,459						
; PRIOR FILING DATE: 2001-04-23						
; PRIOR APPLICATION NUMBER: PCT/US01/03537						
; PRIOR FILING DATE: 2001-02-02						
; PRIOR APPLICATION NUMBER: 09/497,625						
; PRIOR FILING DATE: 2000-02-03						
; PRIOR APPLICATION NUMBER: 09/359,193						
; PRIOR FILING DATE: 1999-07-22						
; PRIOR APPLICATION NUMBER: 09/121,781						
; PRIOR FILING DATE: 1998-07-23						
; NUMBER OF SEQ ID NOS: 107						
; SOFTWARE: FastSeq for Windows Version 3.0						
; SEQ ID NO 55						
; LENGTH: 112						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
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Qy	1 FTLEISR 7					
Db	76 FTLEISR 82					
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; Sequence 55, Application US/10733563						
; Publication No. US2004015172A1						
; GENERAL INFORMATION:						
; APPLICANT: O'Keefe, Theresa						
; APPLICANT: Ponath, Paul						
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND						
; FILE REFERENCE: 10448-213001						
; CURRENT APPLICATION NUMBER: US/10/733,563						
; CURRENT FILING DATE: 2003-12-10						
; PRIOR APPLICATION NUMBER: US 10/272,899						
; PRIOR FILING DATE: 2002-10-17						
; PRIOR APPLICATION NUMBER: US 60/392,364						
; PRIOR FILING DATE: 2002-06-26						
; PRIOR APPLICATION NUMBER: US 60/350,166						
; PRIOR FILING DATE: 2001-10-19						
; NUMBER OF SEQ ID NOS: 122						
; SOFTWARE: FastSeq for Windows Version 4.0						
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Db	76 FTLEISR 82					
RESULT 12						
US-09-940-727B-5						
; Sequence 5, Application US/09940727B						
; Publication No. US2003007793A1						
; GENERAL INFORMATION:						
; APPLICANT: Landry, Donald W						
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY						
; FILE REFERENCE: 0575/51400-B						
; CURRENT APPLICATION NUMBER: US/09/940,727B						
; CURRENT FILING DATE: 2002-09-04						
; PRIOR APPLICATION NUMBER: 09/214,095						
; PRIOR FILING DATE: 1998-12-28						
; PRIOR APPLICATION NUMBER: PCT/US97/10965						
; PRIOR FILING DATE: 1997-06-25						
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; PRIOR FILING DATE: 1996-06-25						
; NUMBER OF SEQ ID NOS: 121						
; SOFTWARE: PatentIn version 3.1						
; SEQ ID NO 5						
; LENGTH: 113						
; TYPE: PRT						
; ORGANISM: mouse						
US-09-940-727B-5						
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Best Local Similarity		100.0%;	Pred. No. 20;			
Matches		7;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Qy	1 FTLEISR 7					
Db	76 FTLEISR 82					
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US-09-940-727B-6						
; Sequence 6, Application US/09940727B						
; Publication No. US2003007793A1						
; GENERAL INFORMATION:						
; APPLICANT: Landry, Donald W						
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY						
; FILE REFERENCE: 0575/51400-B						
; CURRENT APPLICATION NUMBER: US/09/940,727B						
; CURRENT FILING DATE: 2002-09-04						
; PRIOR APPLICATION NUMBER: 09/214,095						
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; PRIOR APPLICATION NUMBER: PCT/US97/10965						
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; NUMBER OF SEQ ID NOS: 121						
; SOFTWARE: PatentIn version 3.1						
; SEQ ID NO 6						
; LENGTH: 113						
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; ORGANISM: mouse						
US-09-940-727B-6						
Query Match		100.0%;	Score 33;	DB 10;	Length 113;	
Best Local Similarity		100.0%;	Pred. No. 20;			
Matches		7;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Qy	1 FTLEISR 7					
Db	76 FTLEISR 82					

Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Search completed: November 4, 2004, 01:13:29
Job time : 73.3333 secs

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14
US-09-940-727B-7
; Sequence 7, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-7

Query Match 100.0%; Score 33; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 15
US-09-940-727B-8
; Sequence 8, Application US/09940727B
; Publication No. US20030077793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-8

Query Match 100.0%; Score 33; DB 10; Length 113;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:44:39 ; Search time 286.667 Seconds
(without alignments)
27.056 Million cell updates/sec

Title: US-09-712-819D-12
Perfect score: 33
Sequence: 1 FTLEISR 7

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Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA Main:*

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SUMMARIES

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2	33	100.0	7	21	US-09-712-819D-12	Sequence 12, Appl
3	33	100.0	32	1	PCT-US04-20295-104	Sequence 104, App
4	33	100.0	32	1	PCT-US04-20564-104	Sequence 104, App
5	33	100.0	32	29	US-10-327-598-401	Sequence 401, App
6	33	100.0	32	29	US-10-327-598-403	Sequence 403, App
7	33	100.0	32	34	US-10-877-773-104	Sequence 104, App
8	33	100.0	32	34	US-10-877-774-104	Sequence 104, App
9	33	100.0	74	22	US-09-791-537-56094	Sequence 56094, A
10	33	100.0	75	22	US-09-791-537-56094	Sequence 56094, A
11	33	100.0	100	1	PCT-US01-03537-32	Sequence 133183, A
12	33	100.0	100	1	PCT-US03-39599A-32	Sequence 32, Appl
13	33	100.0	100	33	US-10-733-563-32	Sequence 32, Appl
14	33	100.0	100	33	US-10-766-610-32	Sequence 32, Appl
15	33	100.0	100	33	US-10-766-610-32	Sequence 32, Appl
16	33	100.0	104	23	US-09-834-366-18009	Sequence 18009, A
17	33	100.0	104	36	US-09-197-873-18009	Sequence 18009, A
18	33	100.0	111	30	US-10-466-242-48	Sequence 48, Appl
19	33	100.0	112	1	PCT-US01-03537-55	Sequence 55, Appl
20	33	100.0	112	1	PCT-US03-39599A-55	Sequence 55, Appl
21	33	100.0	112	1	PCT-US04-20295-19	Sequence 19, Appl
22	33	100.0	112	1	PCT-US04-20564-19	Sequence 19, Appl
23	33	100.0	112	33	US-10-733-563-55	Sequence 55, Appl
24	33	100.0	112	33	US-10-766-610-55	Sequence 55, Appl
25	33	100.0	112	33	US-10-766-610-55	Sequence 55, Appl
26	33	100.0	112	34	US-10-877-773-19	Sequence 19, Appl
27	33	100.0	112	34	US-10-877-774-19	Sequence 19, Appl
28	33	100.0	113	1	PCT-US03-21304-88	Sequence 88, Appl
29	33	100.0	113	1	PCT-US04-17118-14	Sequence 14, Appl
30	33	100.0	113	10	US-08-672-345A-5	Sequence 5, Appl
31	33	100.0	113	10	US-08-672-345A-6	Sequence 6, Appl
32	33	100.0	113	10	US-08-672-345A-7	Sequence 7, Appl
33	33	100.0	113	10	US-08-672-345A-8	Sequence 8, Appl
34	33	100.0	113	24	US-09-940-727B-5	Sequence 5, Appl
35	33	100.0	113	24	US-09-940-727B-6	Sequence 6, Appl
36	33	100.0	113	24	US-09-940-727B-7	Sequence 7, Appl
37	33	100.0	113	24	US-09-940-727B-8	Sequence 8, Appl
38	33	100.0	113	24	US-09-940-727B-100	Sequence 100, App
39	33	100.0	113	24	US-09-940-727B-104	Sequence 104, App
40	33	100.0	113	24	US-09-940-727B-108	Sequence 108, App
41	33	100.0	113	24	US-09-940-727B-112	Sequence 112, App
42	33	100.0	119	26	US-10-049-868-3	Sequence 3, Appl
43	33	100.0	119	26	US-10-049-868-3	Sequence 3, Appl
44	33	100.0	121	3	US-07-868-983-6	Sequence 6, Appl
45	33	100.0	122	1	PCT-US99-24443-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-712-819-12
; Sequence 12, Application US/09712819
; GENERAL INFORMATION:
; APPLICANT: Stevens, Fred J.
; Argon, Yair
; Davis, David P.
; Raffan, Rosemarie
; TITLE OF INVENTION: Fibril-Blocking Peptide, A Method for Preventing
; Fibril Formation
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHERSKOV & FLAYNIK
; STREET: 20 N. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R, 700 MB storage

APPLICANT: Feng, Xiao
APPLICANT: Foord, Orit
APPLICANT: Green, Larry
APPLICANT: Gudas, Jean
APPLICANT: Keyt, Bruce
APPLICANT: Liu, Ying
APPLICANT: Rathanaswami, Palani
APPLICANT: Raya, Robert
APPLICANT: Yang, Xiao Dong
APPLICANT: Corvalan, Jose
APPLICANT: Foltz, Ian
APPLICANT: Jia, Xiao-Chi
APPLICANT: Kang, Jaspal
APPLICANT: King, Chadwick T.
APPLICANT: Klakamp, Scott L.
APPLICANT: Su, Qiaojuan Jane
TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
FILE REFERENCE: AGENIX.087VPC2
CURRENT FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: PCT/US04/20564
PRIOR FILING DATE: 2004-07-06
PRIOR APPLICATION NUMBER: US 60/483,145
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 60/525,570
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: US 60/562,453
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide sequence
PCT-US04-20564-104

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 5
US-10-327-598-401
Sequence 401, Application US/10327598
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: for Making and Using Them
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 401
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-401

Query Match 100.0%; Score 33; DB 29; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 6
US-10-327-598-403
Sequence 403, Application US/10327598
GENERAL INFORMATION:
APPLICANT: Krah, Eugene
APPLICANT: Guo, Honliang
APPLICANT: Aiyappa, Ashok
APPLICANT: Lawton, Robert
TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
TITLE OF INVENTION: for Making and Using Them
FILE REFERENCE: 01-799-A
CURRENT APPLICATION NUMBER: US/10/327,598
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/344,874
PRIOR FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 1139
SOFTWARE: PatentIn version 3.0
SEQ ID NO 403
LENGTH: 32
TYPE: PRT
ORGANISM: canis familiaris;
US-10-327-598-403

Query Match 100.0%; Score 33; DB 29; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 7
US-10-877-773-104
Sequence 104, Application US/10877773
GENERAL INFORMATION:
APPLICANT: Weber, Richard
APPLICANT: Feng, Xiao
APPLICANT: Foord, Orit
APPLICANT: Green, Larry
APPLICANT: Gudas, Jean
APPLICANT: Keyt, Bruce
APPLICANT: Liu, Ying
APPLICANT: Rathanaswami, Palani
APPLICANT: Raya, Robert
APPLICANT: Yang, Xiao Dong
APPLICANT: Corvalan, Jose
APPLICANT: Foltz, Ian
APPLICANT: Jia, Xiao-Chi
APPLICANT: Kang, Jaspal
APPLICANT: King, Chadwick T.
APPLICANT: Klakamp, Scott L.
APPLICANT: Su, Qiaojuan Jane
TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF
FILE REFERENCE: AGENIX.087A
CURRENT APPLICATION NUMBER: US/10/877,773
CURRENT FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: 60/483,145
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/525,570
PRIOR FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/562,453
PRIOR FILING DATE: 2004-04-15
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 104
LENGTH: 32

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide sequence
US-10-877-773-104

Query Match 100.0%; Score 33; DB 34; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 8
US-10-877-774-104
; Sequence 104, Application US/10877774

; GENERAL INFORMATION:
; APPLICANT: Weber, Richard
; APPLICANT: Feng, Xiao
; APPLICANT: Foord, Orit
; APPLICANT: Green, Larry
; APPLICANT: Gudas, Jean
; APPLICANT: Keyt, Bruce
; APPLICANT: Liu, Ying
; APPLICANT: Rathanaswami, Palani
; APPLICANT: Raya, Robert
; APPLICANT: Yang, Xiao Dong
; APPLICANT: Corvalan, Jose
; APPLICANT: Foltz, Ian
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Kang, Jaspal
; APPLICANT: King, Chadwick T.
; APPLICANT: Klakamp, Scott L.
; APPLICANT: Su, Qiaojuan Jane

; TITLE OF INVENTION: ANTIBODIES DIRECTED TO THE DELETION
; TITLE OF INVENTION: MUTANTS OF EPIDERMAL GROWTH FACTOR RECEPTOR AND USES THEREOF

; FILE REFERENCE: ABGENIX.087A2
; CURRENT APPLICATION NUMBER: US/10/877,774
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: 60/483,145
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/525,570
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/562,453
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 32
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic peptide sequence
US-10-877-774-104

Query Match 100.0%; Score 33; DB 34; Length 32;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 15 FTLEISR 21

RESULT 9
US-09-791-537-56094
; Sequence 56094, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56094
; LENGTH: 74
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-791-537-56094

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Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 45 FTLEISR 51

RESULT 10

US-09-791-537-133183
; Sequence 133183, Application US/09791537

; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 133183
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-133183

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Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 51 FTLEISR 57

RESULT 11

PCT-US01-03537-32
; Sequence 32, Application PC/TUS0103537
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052005
; CURRENT APPLICATION NUMBER: PCT/US01/03537
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23

; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-03537-32

Query Match 100.0%; Score 33; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 12
PCT-US03-39599A-32
; Sequence 32, Application PC/TUS0339599A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213W01
; CURRENT APPLICATION NUMBER: PCT/US03/39599A
; PRIOR FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-39599A-32

Query Match 100.0%; Score 33; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 13
US-10-733-563-32
; Sequence 32, Application US/10733563
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 10448-213001
; CURRENT APPLICATION NUMBER: US/10/733,563
; PRIOR FILING DATE: 2003-12-10
; PRIOR FILING DATE: 2002-10-17
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2002-06-26
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-733-563-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 14
US-10-766-610-32
; Sequence 32, Application US/10766610
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-029
; CURRENT APPLICATION NUMBER: US/10/766,610
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/840,459
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-766-610-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLEISR 7
Db 76 FTLEISR 82

RESULT 15
US-10-766-773-32
; Sequence 32, Application US/10766773
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-028
; CURRENT APPLICATION NUMBER: US/10/766,773
; CURRENT FILING DATE: 2004-01-27
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT

; ORGANISM: Mus musculus
US-10-766-773-32

Query Match 100.0%; Score 33; DB 33; Length 100;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLEISR 7
| | | | |
Db 76 FTLEISR 82

Search completed: November 4, 2004, 01:09:18
Job time : 287.667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:01:08 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	45.5	7	2	S19630
2	13	39.4	7	2	A28709
3	12	36.4	5	2	T14910
4	11	33.3	5	2	P06644
5	10	30.3	7	2	P80254
6	9	27.3	3	3	T13892
7	9	27.3	4	2	T46627
8	9	27.3	4	2	I40804
9	9	27.3	5	2	A44955
10	9	27.3	5	2	S11127
11	9	27.3	5	2	P07525
12	9	27.3	5	2	P07577
13	9	27.3	5	2	P07000
14	9	27.3	5	2	S69237
15	9	27.3	5	2	A60521
16	9	27.3	5	2	E42364
17	9	27.3	5	2	P07565
18	9	27.3	6	2	A60986
19	9	27.3	6	2	A43766
20	9	27.3	6	2	I37263
21	9	27.3	6	2	B62606
22	9	27.3	6	2	I65546
23	9	27.3	6	2	PT0518
24	9	27.3	6	2	PT0662
25	9	27.3	6	2	I49424
26	9	27.3	7	2	JN0859
27	9	27.3	7	2	B39127
28	9	27.3	7	2	S25266
29	9	27.3	7	2	PN0150

30 9 27.3 7 2 S78024 ribosomal protein
31 9 27.3 7 2 E48394 glycoprotein compo
32 9 27.3 7 2 I48086 DNA topoisomerase
33 9 27.3 7 2 PT0671 T-cell receptor be
34 9 27.3 7 2 S66442 glutathione S-tran
35 9 27.3 7 2 B48394 major fat-globule
36 9 27.3 7 2 PN0649 pullulanase (BC 3.
37 9 27.3 7 2 S09066 globulin IV alpha
38 9 27.3 7 2 A15398 choline oxidase (E
39 9 27.3 7 2 A25269 sex pheromone CCM3
40 9 27.3 7 2 A30812 sex pheromone cCfl
41 8 24.2 4 2 I40505 hypothetical prote
42 8 24.2 5 2 I39964 ribosomal protein
43 8 24.2 5 2 I39966 ribosomal protein
44 8 24.2 5 2 I39965 ribosomal protein
45 8 24.2 5 2 B22565 R-phycoerythrin al

ALIGNMENTS

RESULT 1

S19630
ribosomal protein L30 - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C:Accession: S19630
R:Ochi, K.

Int. J. Syst. Bacteriol. 42, 144-150, 1992

A>Title: Electrophoretic heterogeneity of ribosomal protein Ar-L30 among actinomycete s
A:Reference number: S19630; MUID:92144363; PMID:1736962

A:Accession: S19630

A:Molecule type: protein

A:Residues: 1-7 <OCH>

A:Experimental source: strain IFO 13189

C:Superfamily: Escherichia coli ribosomal protein L30

C:Keywords: protein biosynthesis; ribosome

Query Match 45.5%; Score 15; DB 2; Length 7;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKISR 7

Db 3 LKITQ 7

RESULT 2

A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C:Species: Bacillus cereus

C>Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C:Accession: A28709

R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.

Biochemistry 27, 2223-2234, 1988

A>Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
due.

A:Reference number: A28709; MUID:88241058; PMID:3132206

A:Accession: A28709

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <OLS>

Query Match 39.4%; Score 13; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKI 5

Db 1 LKI 3

RESULT 3

Tl4910
hypothetical protein - parsley
C:Species: Petroselinum crispum (parsley)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: Tl4910
R:Kircher, S.; Ledger, S.; Hayashi, H.; Weishaar, B.; Schafer, B.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 593-605, 1998
A:Title: CPRF4, a novel plant bZIP protein of the CPRF family: comparative analysis of
A:Reference number: Z18261; MUID:98265918; PMID:9604882
A:Accession: Tl4910
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-5 <KIR>
A:Cross-references: EMBL:Y10810; NID:G3336904; PIDN:CAA71769.1; PID:G3336905
A:Experimental source: ssp. Hamburger Schnitt

Query Match 36.4%; Score 12; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
:||
Db 2 VSR 4

RESULT 4
PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0644
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0644
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Cross-references: UNIPROT:Q92276
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
:||
Db 4 FT 5

RESULT 5
PS0254
18K protein 5507 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C:Accession: PS0254
R:Tsuigita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0254
A:Molecule type: protein
A:Residues: 1-7 <TSU>
A:Experimental source: leaf, chloroplast, strain Nihonbare
A>Note: molecular weight 18K, pI 4.4

Query Match 30.3%; Score 10; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKISR 7
:|:|:

Db 1 LAIAK 5

RESULT 6
Tl3892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fra
C:Species: mitochondrion Lampetra fluviatilis (river lamprey)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: Tl3892
R:Delarbre, C.; Barriol, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A:Title: The main features of the craniate mitochondrial DNA between the NDI and the CO
A:Reference number: Z17775; MUID:97398704; PMID:9254918
A:Accession: Tl3892
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3
A:Cross-references: EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123
C:Genetics:
A:Genome: mitochondrion
A>Note: COI
C:Keywords: mitochondrion; oxidoreductase

Query Match 27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
:||
Db 2 TL 3

RESULT 7
T46627
hypothetical protein c4 - loblolly pine
C:Species: Pinus taeda (loblolly pine)
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: T46627
R:Chang, S.; Purves, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is
A:Reference number: Z23105
A:Accession: T46627
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <CHA>
A:Cross-references: EMBL:U31309; NID:G974285; PID:G974292
A:Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 27.3%; Score 9; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LKI 5
:|:
Db 1 MKL 3

RESULT 8
I40804
endoglucanase F - Clostridium thermocellum (fragment)
C:Species: Clostridium thermocellum
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40804
R:Wishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 1991
A:Title: Transcription of clostridium thermocellum endoglucanase genes celf and celd.
A:Reference number: I40804; MUID:91100322; PMID:1987137
A:Accession: I40804
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RES>
A:Cross-references: UNIPROT:P26224; GB:M64363; NID:G144771

C:Genetics:
A:Gene: celf
A:Start codon: TTG

Query Match 27.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KI 5
||
Db 3 KI 4

RESULT 9
A4955
alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)
C:Species: Vibrio harveyi
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C:Accession: A44955
R:Paquette, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A:Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
A:Reference number: A44955; MUID:90175700; PMID:2626493
A:Accession: A44955
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <PAQ>
C:Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
||
Db 3 IXR 5

RESULT 10
S11127
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C:Accession: S11127; S11128
R:Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. J. 268, 585-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identification o
A:Reference number: S11127; MUID:90303246; PMID:2363696
A:Accession: S11127
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <MIK1>
A:Accession: S11128
A>Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 2-5 <MIK2>
C:Keywords: phosphoprotein

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
||
Db 3 VSK 5

RESULT 11
PT0525
T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0525

R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0525
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
||
Db 2 SR 3

RESULT 12
PT0577
T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0577; PT0574
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0577
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
A:Accession: PT0574
A:Molecule type: mRNA
A>Status: translation not shown
A:Residues: 1-5 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7
||
Db 3 SR 4

RESULT 13
PT0700
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0700
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0700
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7

Db ||
3 SR 4

RESULT 14
S69237
surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C:Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Peters, J.; Nitsch, M.; Kuehlmoergen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
J. Mol. Biol. 245, 385-401, 1995
A:Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua
A:Reference number: S69237; PMID:95139068; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <P>
A:Experimental source: strain F1, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
Db 2 TL 3

RESULT 15
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Mar-2004
C:Accession: A60521
R:Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A:Reference number: A60521; PMID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5
C:Keywords: Glycyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIS 6
:||
Db 1 QIS 3

Search completed: November 4, 2004, 07:10:22
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:53:12 ; Search time 188 Seconds
(without alignments)
21.424 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	13	39.4	6	P82181	P82181 spinacia ol
2	13	39.4	6	P82182	P82182 spinacia ol
3	11	33.3	5	RE31_LITRU	P82072 litorea rub
4	11	33.3	5	RE32_LITRU	P82073 litorea rub
5	11	33.3	7	Q95945	Q95945 saccharomyc
6	11	33.3	7	Q95945	P83530 lactobacill
7	10	30.3	6	P82541	P82541 spinacia ol
8	10	30.3	7	GFRP_MOUSE	P99025 mus musculu
9	9	27.3	4	Q08433	Q08433 rattus sp.
10	9	27.3	5	UN06_MOUSE	P38639 mus musculu
11	9	27.3	6	UN06_MOUSE	P81351 clostridium
12	9	27.3	7	CCFL_ENTFA	P20104 enterococcu
13	9	27.3	7	CHON_ALGSP	P16101 alcaligenes
14	9	27.3	7	CIA_ENTFA	P11932 enterococcu
15	9	27.3	7	U224_MAIZE	P80630 zea mays (m
16	9	27.3	7	Q15897	Q15897 homo sapien
17	9	27.3	7	P93233	P93233 lycopersico
18	9	27.3	7	Q07354	Q07354 synechococc
19	9	27.3	7	Q8GL00	Q8GL00 borrelia bu
20	9	27.3	7	Q8GL04	Q8GL04 borrelia bu
21	9	27.3	7	Q8GL12	Q8GL12 borrelia bu
22	9	27.3	7	O55184	O55184 rattus norv
23	9	27.3	7	Q63480	Q63480 rattus norv
24	9	27.3	7	Q8K3H6	Q8K3H6 rattus norv
25	9	27.3	7	Q8JEB1	Q8JEB1 human immun
26	8	24.2	5	ALL14_CARMA	P81817 carcinus ma
27	8	24.2	5	PSK_DAUCA	P58261 daucus caro
28	8	24.2	7	ALL2_CARMA	P81805 carcinus ma
29	8	24.2	7	ALL3_CARMA	P81806 carcinus ma
30	8	24.2	7	ALL4_CARMA	P81807 carcinus ma
31	8	24.2	7	ALL5_CARMA	P81808 carcinus ma

32	8	24.2	7	1	ALL7_CVDPO	P82158 cydia pomon
33	8	24.2	7	1	CARP_MITED	P10420 mytilus edu
34	8	24.2	7	1	FARS_HIRME	P42564 hirudo medi
35	8	24.2	7	2	P70804	P70804 azotobacter
36	8	24.2	7	2	Q47029	Q47029 enterobacte
37	8	24.2	7	2	Q9YIO9	Q9YIO9 human adeno
38	8	24.2	7	2	Q9YIRO	Q9YIRO human adeno
39	8	24.2	7	2	Q9YVE3	Q9YVE3 human adeno
40	7	21.2	3	1	LUXE_VIBFI	P24272 vibrio fisc
41	7	21.2	5	2	P83073	P83073 bacillus ce
42	7	21.2	6	1	LOX1_LOCMI	P41491 locusta mig
43	7	21.2	6	1	VP19_HVLIK	P23210 human herpe
44	7	21.2	7	2	Q8NH7	Q8NH7 homo sapien
45	7	21.2	7	2	Q8TAQ4	Q8TAQ4 homo sapien

ALIGNMENTS

RESULT 1
P82181
ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_taxid=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 kDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 63218415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ISR 7
Db 2 ISR 4

RESULT 2
P82182
ID P82182 PRELIMINARY; PRT; 6 AA.
AC P82182;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. ALVARO; TISSUE=leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDa.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002363; Ribosomal_L10eub.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISR 7
Db 2 ISR 4

RESULT 3
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion.
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=PAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 4
RE32_LITRU
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
Db 4 FT 5

RESULT 5
Q95945
ID Q95945 PRELIMINARY; PRT; 7 AA.
AC Q95945;
DT 01-FEB-1997 (TREMELrel. 02, Created)
DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
RA Bonitz S.G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KIS 6
Db 5 KLS 7

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KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 30.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLK 4
DB 3 SLK 5

RESULT 6
P83530 PRELIMINARY; PRT; 7 AA.
ID AC P83530
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLK 5
DB 2 TLDV 5

RESULT 7
P82541 PRELIMINARY; PRT; 6 AA.
ID AC P82541
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=cv. ALVARO; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PT. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 kDa.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0019843; F:rRNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR02222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.

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KW Chloroplast; Ribosomal protein; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 30.3%; Score 10; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLK 4
DB 3 SLK 5

RESULT 8
GFRP_MOUSE STANDARD; PRT; 7 AA.
ID AC GFRP_MOUSE
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN Name=Gchfr; Synonyms=Girp;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Van J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
RL Submitted (AUG-1998) to Swiss-Prot.
CC -!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
DR SWISS-2DPAGE; P99025; MOUSE.
KW Direct protein sequencing.
FT INIT_MET 0
FT NON_TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LKIS 6
DB 3 LLIS 6

RESULT 9
Q08433 PRELIMINARY; PRT; 4 AA.
ID AC Q08433
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.

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KW Transferase.
FT NON TER 4 473 MW; 633732C420000000 CRC64;
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 27.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LK 4
DB 3 LK 4

RESULT 10
UF01 MOUSE
ID UF01 MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISUE=Fibroblast; PubMed=7523108;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familiar and novel murine proteins using
preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 6.6, its MW is: 19 kDa.
KW Direct protein sequencing.
FT NON TER 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ISR 7
DB 2 IGR 4

RESULT 11
UN06 CLOPA
ID UN06 CLOPA STANDARD; PRT; 6 AA.
AC P81351;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 6 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjelvald L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-805(1998).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 5.0, its MW is: 75.9 kDa.
KW Direct protein sequencing.
FT NON TER 6
SQ SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLKI 5
DB 3 TAEI 6

RESULT 12
CCF1 ENTFA
ID CCF1 ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
transfer of the Streptococcus faecalis tetracycline resistance
plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
hemolysin plasmid pCF10.
DR PIR: A30812; A30812.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
DB 3 TL 4

RESULT 13
CHOX ALCSP
ID CHOX ALCSP STANDARD; PRT; 7 AA.
AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR: A15398; A15398.
KW Direct protein sequencing; Oxidoreductase.
FT NON TER 7
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 SR 7 27.3%; Score 9; DB 1; Length 7;
 ||| Best Local Similarity 66.7%; Pred.No. 1.8e+06;
 Db 6 SR 7 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TLK 4
 |||
 Db 2 TAK 4

Search completed: November 4, 2004, 07:09:40
 Job time : 190 secs

RESULT 14
 CIA_ENTFA STANDARD; PRT; 7 AA.
 ID UC24_MAIZE
 AC P11932;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=87005252; PubMed=3093276;
 RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
 RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
 RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
 RT CAM373";
 RL FEBS Lett. 206:69-72(1986).
 CC -!- FUNCTION: CAM373 induces mating response of donor cells harboring
 CC PAM373.
 CC -!- MISCELLANEOUS: The N-terminus is possibly responsible for
 CC specificity of pheromones to plasmids.
 CC PIR; A25269; A25269.
 DR Direct protein sequencing; Pheromone.
 KW
 SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 7;
 Best Local Similarity 66.7%; Pred.No. 1.8e+06;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTL 3
 |||
 Db 3 FIL 5

RESULT 15
 UC24_MAIZE STANDARD; PRT; 7 AA.
 ID UC24_MAIZE
 AC P80630;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 447)
 DE (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Parnollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 6.0, its MW is: 30.0 kDa.
 DR Maize-2DPAGE; P80630; COLEOPTILE.
 DR MaizeDB; 123956; -.
 KW Direct protein sequencing.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:52:27 ; Search time 152 seconds
(without alignments)
16.520 Million cell updates/sec

Title: US-09-712-819D-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	69.7	7	2	Aay40736 S4 deriva
2	23	69.7	7	3	Aab30074 Scaffold
3	22	66.7	7	2	Aay40738 S4 deriva
4	22	66.7	7	3	Aab30076 Scaffold
5	21	63.6	7	2	Aay42013
6	20	60.6	7	2	AAR81848
7	20	60.6	7	2	AAY41889
8	20	60.6	7	4	ABB55870
9	20	60.6	7	4	ABB56283
10	20	60.6	7	4	ABB55981
11	20	60.6	7	4	AAU28602
12	20	60.6	7	4	AAU24969
13	20	60.6	7	4	AAU26249
14	20	60.6	7	4	AAU15313
15	20	60.6	7	4	ABB52190
16	20	60.6	7	4	ABB52355
17	20	60.6	7	5	ABG78901
18	20	60.6	7	5	ABG78730
19	20	60.6	7	6	ABP58010
20	20	60.6	7	6	ABP57255
21	20	60.6	7	6	ABP57203
22	20	60.6	7	6	ABR59010
23	20	60.6	7	6	ABR59042
24	20	60.6	7	8	ADH35821
25	20	60.6	7	8	ADH35827

ALIGNMENTS

RESULT 1

RAY40736

ID AAY40736 standard; peptide; 7 AA.

XX AC AAY40736;

XX AC

DT 01-DEC-1999 (first entry)

XX

DE S4 derivative #10, beta strand of scaffold protein structure.

XX

KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;

KW tumour; chemotherapeutic agent.

XX

OS Synthetic.

XX

FN EP947582-A1.

XX

PD 06-OCT-1999.

XX

PF 31-MAR-1998; 98EP-00870065.

XX

PR 31-MAR-1998; 98EP-00870065.

XX

PA (INNO-) INNOGENETICS NV.

XX

PI Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX

PT New scaffold protein, useful for stabilizing antigens used as vaccines.

XX

PS Disclosure; Page 6; 105pp; English.

XX

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 69.7%; Score 23; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTILKIS 6
DB 2 FTILSIS 7

RESULT 2
AAB30074
ID AAB30074 standard; peptide; 7 AA.
XX
AC AAB30074;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
PN WO200060070-A1.
XX
PD 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP002283.
XX
PR 01-APR-1999; 99WO-EP002283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 2000-665002/64.
XX
PT Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
PS Disclosure; Page 15; 68pp; English.
XX
CC The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC the invention
XX
SQ Sequence 7 AA;

Query Match 69.7%; Score 23; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTILKIS 6
DB 2 FTILSIS 7

RESULT 4

Db 2 FTILSIS 7

RESULT 3
AAY40738
ID AAY40738 standard; peptide; 7 AA.
XX
AC AAY40738;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #12, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
PN EP947582-A1.
XX
PD 06-OCT-1999.
XX
PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
DR WPI; 1999-542958/46.
XX
PT New scaffold protein, useful for stabilizing antigens used as vaccines.
XX
PS Disclosure; Page 6; 105pp; English.
XX
CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 66.7%; Score 22; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTILKIS 6
DB 2 FTILSIS 7

RESULT 4

AAE30076	standard; peptide; 7 AA.
AAE30076	AAE30076;
09-FEB-2001	(first entry)
Scaffold protein SCA S4	peptide SEQ ID NO: 137.
Human; CTLA-4;	scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
Synthetic.	
WO200060070-A1.	
12-OCT-2000.	
01-APR-1999;	99WO-EP002283.
01-APR-1999;	99WO-EP002283.
(INNO-) INNOGENETICS NV.	
Desmet J, Hufton S, Hoogenboom H, Sablon E;	
WPI; 2000-665002/64.	
Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.	
Disclosure; Page 15; 68pp; English.	
The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAE29930-B29939 were used in the production of the proteins of the invention	
Sequence 7 AA;	
Query Match	66.7%; Score 22; DB 3; Length 7;
Best Local Similarity	83.3%; Pred. No. 1.7e+06;
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 FTLKIS 6
Db	2 FTLTIS 7
RESULT 5	
AAE42013	AAE42013 standard; peptide; 7 AA.
ID	AAE42013 standard; peptide; 7 AA.
AC	AAE42013;
DT	09-DEC-1999 (first entry)
DE	Rheumatoid arthritis diagnostic protein isoform peptide #164.
XX	Human; rheumatoid arthritis; RA; diagnosis; RPI; RADP; detection; rheumatoid arthritis diagnostic feature; RPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
OS	Homo sapiens.
XX	
PN	WO9947925-A2.
XX	

XX 31-MAR-1995; 95WO-US004075.
XX PF
XX 31-MAR-1994; 94US-00222619.
XX PR
XX (AMGE-) AMGEN INC.
XX PA
XX (UYRQ) UNIV ROCKEFELLER.
XX PA
XX Lichenstein HS, Lyons DE, Wurfel MM, Wright SD;
XX PI
XX WPI; 1995-358634/46.
XX DR
XX Human afamin or a variant and polynucleotide(s) encoding it - a human
XX PT
XX serum protein with activities in common with other members of this
XX PT
XX family.
XX
XX Example 3; Page 45; 97pp; English.
XX PS
XX Peptides AAR81847-54 are tryptic peptide fragments from human afamin
XX CC
XX (AAR81845) novel member of the human serum protein family. The fragments
XX CC
XX were used to design primers and probes (AAR00786-98) for the cloning of
XX CC
XX the afamin gene (AAY00785) from human liver cDNA. Afamin is thought to
XX CC
XX have similar properties to human albumin, alpha-fetoprotein and vitamin
XX CC
XX D binding protein due to homology with these proteins. The gene encodes a
XX CC
XX mature protein of 68576 daltons without post-translational processing
XX CC
XX (ca. 87000 daltons with post-translational processing). The protein was
XX CC
XX isolated from human plasma by a conventional chromatographic methods. The
XX CC
XX protein can be used to ameliorate ischaemia-reperfusion injury,
XX CC
XX rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma
XX CC
XX substances released after inflammation, etc
XX CC
XX Sequence 7 AA;
XX SQ

Query Match 60.6%; Score 20; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|| : ||
Db 1 FTFEYSR 7

RESULT 7
AAY41889
ID AAY41889 standard; peptide; 7 AA.
XX AC
XX AAY41889;
XX DT
XX 09-DEC-1999 (first entry)
XX DE
XX Rheumatoid arthritis diagnostic protein isoform peptide #40.
XX DE
XX Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
XX KW
XX rheumatoid arthritis diagnostic feature; ERPI; synovial fluid;
XX KW
XX rheumatoid arthritis diagnostic protein isoform; screening;
XX KW
XX expression reference protein isoform; prognosis.
XX XX
XX Homo sapiens.
XX OS
XX WO9947925-A2.
XX PN
XX 23-SEP-1999.
XX PD
XX 15-MAR-1999; 99WO-GB000763.
XX PF
XX 13-MAR-1998; 98GB-00005477.
XX PR
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA
XX Parekh RB, Patel TP, Townsend RR;
XX PI
XX WPI; 1999-571871/48.
XX DR
XX
XX PT

PT Diagnosis of human rheumatoid arthritis by two-dimensional
PT electrophoresis.
XX
XX Disclosure; Page 18; 157pp; English.
XX PS
XX A method has been developed for the diagnosis of human rheumatoid
XX CC
XX arthritis (RA) using two-dimensional electrophoresis to generate a two-
XX CC
XX dimensional array of features. The method can be used for screening,
XX CC
XX diagnosis and prognosis of RA in a subject or for monitoring the effect
XX CC
XX of an anti-RA drug or therapy administered to a subject. The method
XX CC
XX comprises: (a) analysing a sample of serum or plasma and optionally
XX CC
XX synovial fluid by two-dimensional electrophoresis, to generate a two-
XX CC
XX dimensional array of features; (b) identifying at least one chosen
XX CC
XX feature whose relative abundance correlates with the presence or absence
XX CC
XX of RA; and (c) comparing the abundance of each chosen feature in the
XX CC
XX sample with the abundance of that chosen feature in serum or plasma from
XX CC
XX one or more persons without RA, where the relative abundance of the
XX CC
XX chosen feature or features in the sample indicates the presence or
XX CC
XX absence of RA in the subject. The method can also be used in clinical
XX CC
XX studies for testing drugs for therapy of RA, for purification of RA-
XX CC
XX diagnostic protein isoforms (RPIs), and for production of antibodies to
XX CC
XX RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
XX CC
XX RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
XX CC
XX protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to
XX CC
XX AAY42103 represent expression reference protein isoform peptides and
XX CC
XX AAY25066 to AAZ25068 represent degenerate probes for RPIs, which are all
XX CC
XX used in the exemplification of the present invention
XX SQ
XX Sequence 7 AA;
XX SQ

Query Match 60.6%; Score 20; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|| : ||
Db 1 YTFELSR 7

RESULT 8
ABB55870
ID ABB55870 standard; peptide; 7 AA.
XX ID
XX ABB55870;
XX AC
XX ABB55870;
XX DT
XX 15-FEB-2002 (first entry)
XX DD
XX Vascular dementia-associated protein isoform (VPI) 70.
XX DE
XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
XX KW
XX diagnosis; prognosis; gene therapy.
XX KW
XX Homo sapiens.
XX OS
XX WO200169261-A2.
XX PN
XX 20-SEP-2001.
XX PD
XX 14-MAR-2001; 2001WO-GB001106.
XX PF
XX 15-MAR-2000; 2000GB-00006285.
XX PR
XX 24-NOV-2000; 2000GB-00028734.
XX PR
XX 28-NOV-2000; 2000US-00724391.
XX PR
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PA
XX Herath HMWAC, Parekh RB, Rohlf C;
XX PI
XX WPI; 2001-557937/62.
XX DR
XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for
XX PT
XX determining stage of VD and monitoring the effect of VD therapy,
XX PT

PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 31; 151pp; English.
 XX The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX
 SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. NO. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 9
 ABB56283
 ID ABB56283 standard; peptide; 7 AA.
 AC ABB56283;
 XX 15-FEB-2002 (first entry)
 XX Vascular dementia-associated protein isoform (VPI) 483.
 XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200169261-A2.
 XX 20-SEP-2001.
 XX 14-MAR-2001; 2001WO-GB001106.
 XX 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAC, Parekh RB, Rohlf C;
 XX WPI; 2001-557937/62.

Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.
 XX Claim 6; Page 40; 151pp; English.
 XX The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance

CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the
 CC treatment of VD and for gene therapy
 XX

SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. NO. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
 :||:|
 Db 1 YTFELSR 7

RESULT 10
 ABB55981
 ID ABB55981 standard; peptide; 7 AA.
 AC ABB55981;
 XX 15-FEB-2002 (first entry)
 XX Vascular dementia-associated protein isoform (VPI) 181.
 XX Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
 KW diagnosis; prognosis; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200169261-A2.
 XX 20-SEP-2001.
 XX 14-MAR-2001; 2001WO-GB001106.
 XX 15-MAR-2000; 2000GB-00006285.
 PR 24-NOV-2000; 2000GB-00028734.
 PR 28-NOV-2000; 2000US-00724391.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Herath HMAC, Parekh RB, Rohlf C;

WPI; 2001-557937/62.

Screening, diagnosis or prognosis of vascular dementia (VD), useful for
 PT determining stage of VD and monitoring the effect of VD therapy,
 PT comprises analyzing body fluid by 2-dimensional electrophoresis for
 PT features correlated with VD.

Claim 6; Page 33; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular
 CC Dementia (VD) in a subject comprising analysing body fluid from the
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
 CC features containing at least one chosen feature whose relative abundance
 CC correlates with the presence, absence, stage or severity of VD or
 CC predicts the onset or course of VD, especially detecting in a sample of
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
 CC specification. Detecting VD-associated features and VPI is useful for the
 CC screening, diagnosis or prognosis of VD, for determining the stage or
 CC severity of VD, for identifying a subject at risk of VD or for monitoring
 CC the effect of therapy administered to a subject having VD. Nucleic acids
 CC encoding a VPI or inhibiting the function of a VPI are useful for the

CC treatment of VD and for gene therapy

XX Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 11
AAU28602
ID AAU28602 standard; peptide; 7 AA.

XX AC AAU28602;

XX DT 03-JAN-2002 (first entry)

XX DE DPI tryptic digest peptide #199.

XX KW Human; depression associated protein isoform; tryptic digest peptide;
XX KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
XX KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
XX KW manic-depressive illness; schizoaffective disorder.

XX OS Homo sapiens.

XX PN WO200162787-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB000786.

XX PR 24-FEB-2000; 2000GB-00004412.

XX PR 08-DEC-2000; 2000GB-00030050.

XX PR 12-DEC-2000; 2000US-0254830P.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAL, Parekh RB, Rohlf C, Terrett JA, Tyson XL;

XX DR WPI; 2001-570626/64.

XX PT Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.

XX PS Disclosure; Page 34; 153pp; English.

XX CC The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequences encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), manic-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present invention represents one of the DPI tryptic digest peptides of the present

XX SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 12
AAU24969
ID AAU24969 standard; peptide; 7 AA.

XX AC AAU24969;

XX DT 18-DEC-2001 (first entry)

XX DE Schizophrenia-Associated Protein Isoform (SPI) peptide #198.

XX KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;
XX KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.

XX OS Homo sapiens.

XX PN WO200162785-A2.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-GB000792.

XX PR 24-FEB-2000; 2000GB-00004415.

XX PR 28-DEC-2000; 2000US-00750395.

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI Herath HMAL, Parekh RB, Rohlf C, Terrett JA, Tyson XL;

XX DR WPI; 2001-570624/64.

XX PT New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.

XX PS Disclosure; Page 32; 148pp; English.

XX CC The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia. screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs

XX SQ Sequence 7 AA;

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 13
AAU26249
ID AAU26249 standard; peptide; 7 AA.

XX AC AAU26249;

XX DT 18-DEC-2001 (first entry)

XX DE Depression-Associated Protein Isoform DPI-208.

XX KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
XX KW DP; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;

KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
 KW attention deficient disorder; schizoaffective disorder;
 XX unipolar affective disorder.
 OS Homo sapiens.
 XX WO200163294-A2.
 XX 30-AUG-2001.
 XX 23-FEB-2001; 2001WO-GB000791.
 XX 24-FEB-2000; 2000GB-00004412.
 PR 08-DEC-2000; 2000GB-00030050.
 PR 12-DEC-2000; 2000US-0254830P.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAc, Parekh RB, Rohlf C;
 XX WPI; 2001-582081/65.
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD) or
 PT unipolar depression; or for screening for modulators, comprises a BAD-
 PT associated protein isoform.
 XX Claim 8; Page 34; 163pp; English.
 XX The invention relates to a preparation comprising an isolated Bipolar
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are
 CC used to screen, diagnose or prognose of BAD or unipolar depression,
 CC determine the stage or severity of BAD or unipolar depression, identify a
 CC subject at risk of developing BAD or unipolar depression, or monitor the
 CC effect of therapy in a subject. They are also used to screen for or
 CC identify agents that interact with a DPI. These agents, antibodies
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat
 CC or prevent BAD or unipolar depression. Diseases that can be treated are
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a
 CC unipolar affective disorder. The DPIs are used in proteomics. The
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of
 CC BAD or unipolar depression overcomes the problems of using gene
 CC expression analysis, such as not being able to obtain central nervous
 CC system (CNS) tissue from a living patient under normal circumstances. The
 CC present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
 CC subjects having BAD
 XX Sequence 7 AA;
 SQ
 Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db :|:|:
 1 YTFELSR 7
 RESULT 14
 AAU15313
 ID AAU15313 standard; peptide; 7 AA.
 XX AAU15313;
 AC AAU15313;
 XX 24-OCT-2001 (first entry)
 DT
 XX Schizophrenia-associated isoform peptide #198.
 DE
 XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;
 KW neurological disorder; neuropathy.
 XX Homo sapiens.
 OS
 XX WO200163293-A2.
 PN

XX 30-AUG-2001.
 PD 23-FEB-2001; 2001WO-GB000783.
 XX 24-FEB-2000; 2000GB-00004415.
 XX 28-DEC-2000; 2000US-00750395.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Herath HMAc, Parekh RB, Rohlf C;
 XX WPI; 2001-502868/55.
 XX Diagnosing and monitoring Schizophrenia by detecting the presence of
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein
 PT Isoforms in samples of cerebrospinal fluid.
 XX Claim 6; Page 32; 160pp; English.
 XX The invention relates to methods and compositions for screening,
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting
 CC the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,
 CC immunoassay or hybridisation assay, for diagnosing and monitoring SCH,
 CC studying the effectiveness of treatments and for identifying potential
 CC therapeutic agents. The method is used for (1) screening or diagnosis of
 CC SCH and the relative abundance of at least 1 chosen feature correlates
 CC with the presence or absence of SCH; and (2) monitoring the effect of
 CC therapy administered to a subject with SCH and the relative abundance of
 CC at least 1 chosen feature which correlates with the severity of SCH. The
 CC expression and activity of the SPIs, SPIs and related molecules (e.g.
 CC secondary messengers) are studied to diagnose SCH, monitor the progress
 CC of the disorder and the effectiveness of treatment and as targets to
 CC identify and produce potential therapeutic agents for the treatment of
 CC SCH. The paucity of detectable neurologic defects distinguishes
 CC neuropsychiatric disorders such as SCH from neurological disorders, where
 CC manifestations of anatomical and biochemical changes have been identified
 CC in many cases. Consequently the identification and characterisation of
 CC cellular and/or molecular causative defects and neuropathies are
 CC necessary for improved treatment of neuropsychiatric disorders. AAU15114-
 CC AAU15762 represent the amino acid sequences of schizophrenia-associated
 CC isoforms used in the method of the invention
 XX Sequence 7 AA;
 SQ
 Query Match 60.6%; Score 20; DB 4; Length 7;
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db :|:|:
 1 YTFELSR 7
 RESULT 15
 ABB52190
 ID ABB52190 standard; peptide; 7 AA.
 XX ABB52190;
 AC ABB52190;
 XX 08-FEB-2002 (first entry)
 DT
 XX Human API-146 tryptic digest peptide #1.
 DE
 XX Human; neuroprotective; nootropic; gene therapy; vaccine;
 KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
 KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
 KW Expression Reference Protein Isoform; ERPI; proteolysis.
 XX Homo sapiens.
 OS
 XX WO200175454-A2.
 PN

XX 11-OCT-2001.
XX PD
XX PF
XX PF
XX 03-APR-2001; 2001WO-US010908.
XX 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX Durham KL, Friedman DL, Herath HM, Kimmel LH, Parekh RB;
PI Potter DM, Rohlf C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX WPI; 2001-639384/73.
XX Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX Example; Page 30; 162pp; English.
PS
XX The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 7 AA;
Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 1 FTFEYSR 7
Search completed: November 4, 2004, 07:06:25
Job time : 154 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 07:09:49 ; Search time 140 Seconds
(without alignments)
17.661 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 56374

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	7	9	US-09-791-378-198
2	20	60.6	7	9	US-09-998-909-7
3	20	60.6	7	9	US-09-826-290-205
4	20	60.6	7	9	US-09-826-290-370
5	20	60.6	7	10	US-09-791-393-145
6	20	60.6	7	10	US-09-791-389-145
7	20	60.6	7	11	US-09-791-377-198
8	20	60.6	7	15	US-10-264-309-131
9	20	60.6	7	15	US-10-264-309-460
10	20	60.6	7	15	US-10-601-100-105
11	20	60.6	7	17	US-10-700-340-52
12	20	60.6	7	17	US-10-700-340-154
13	18	54.5	7	9	US-09-996-288-164

Sequence 164, App
Sequence 78, Appl
Sequence 164, Appl
Sequence 39, Appl
Sequence 30, Appl
Sequence 101, App
Sequence 135, App
Sequence 13, Appl
Sequence 135, App
Sequence 88, Appl
Sequence 23, Appl
Sequence 87, Appl
Sequence 396, App
Sequence 1971, Ap
Sequence 3503, Ap
Sequence 3542, Ap
Sequence 3544, Ap
Sequence 20, Appl
Sequence 43, Appl
Sequence 35, Appl
Sequence 96, Appl
Sequence 131, App
Sequence 396, App
Sequence 1971, Ap
Sequence 3503, Ap
Sequence 3542, Ap
Sequence 3544, Ap
Sequence 35, Appl
Sequence 96, Appl
Sequence 131, App

ALIGNMENTS

RESULT 1
US-09-791-378-198
; Sequence 198, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-198

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 2
US-09-998-909-7
; Sequence 7, Application US/0998909
; Patent No. US20020164664A1
; GENERAL INFORMATION:
; APPLICANT: Hlavaty, John

APPLICANT: Briggman, Joseph
TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-998-909-7

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLKISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 3
US-09-826-290-205
Sequence 205, Application US/09826290
Patent No. US2002016468A1
GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
APPLICANT: Kimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlf, Christian
APPLICANT: Silber, B. Michael
APPLICANT: Stiger, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: Townsend, Robert Reid
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 2572-1-001 N2
CURRENT APPLICATION NUMBER: US/09/826,290
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 205
LENGTH: 7
TYPE: PRT
ORGANISM: homo sapien
US-09-826-290-205

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 FTLKISR 7
:|:|:
Db 1 FTPEYSR 7

RESULT 4
US-09-826-290-370
Sequence 370, Application US/09826290
Patent No. US2002016468A1

GENERAL INFORMATION:
APPLICANT: Durham, L. Kathryn
APPLICANT: Friedman, David L.
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
APPLICANT: Kimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlf, Christian
APPLICANT: Silber, B. Michael
APPLICANT: Stiger, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: Townsend, Robert Reid
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 2572-1-001 N2
CURRENT APPLICATION NUMBER: US/09/826,290
CURRENT FILING DATE: 2001-04-30
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 370
LENGTH: 7
TYPE: PRT
ORGANISM: homo sapien
US-09-826-290-370

Query Match 60.6%; Score 20; DB 9; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 FTLKISR 7
:|:|:
Db 1 YTFELSR 7

RESULT 5
US-09-791-393-145
Sequence 145, Application US/09791393
Publication No. US20030032200A1
GENERAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohlf, Christian
TITLE OF INVENTION: Proteins, Genes and Their Use for
TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
TITLE OF INVENTION: and Unipolar Depression
FILE REFERENCE: 2543-1-001 N1
CURRENT APPLICATION NUMBER: US/09/791,393
CURRENT FILING DATE: 2002-01-02
EARLIER APPLICATION NUMBER: GB 0004412.3
EARLIER FILING DATE: 2000-02-24
EARLIER APPLICATION NUMBER: GB 0030050.9
EARLIER FILING DATE: 2000-12-08
EARLIER APPLICATION NUMBER: US 60/254,830
EARLIER FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145
LENGTH: 7
TYPE: PRT
ORGANISM: homo sapien
US-09-791-393-145

Query Match 60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
: ||: ||
Db 1 YTFELSR 7

RESULT 6

US-09-791-389-145
; Sequence 145, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; TITLE OF INVENTION: and Unipolar Depression
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-145

Query Match 60.6%; Score 20; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
: ||: ||
Db 1 YTFELSR 7

RESULT 7

US-09-791-377-198
; Sequence 198, Application US/09791377
; Publication No. US20040110938A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-060-999
; CURRENT APPLICATION NUMBER: US/09/791,377
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 198
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-377-198

Query Match 60.6%; Score 20; DB 11; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
: ||: ||
Db 1 YTFELSR 7

RESULT 8

US-10-264-309-131
; Sequence 131, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 131
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131

Query Match 60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTLKISR 7
: ||: ||
Db 1 PTFEYSR 7

RESULT 9

US-10-264-309-460
; Sequence 460, Application US/10264309
; Publication No. US20040022794A1
; GENERAL INFORMATION:
; APPLICANT: DURHAM, L. KATHRYN
; APPLICANT: FRIEDMAN, DAVID L.
; APPLICANT: HERATH, HERATH
; APPLICANT: KIMMEL, LIDA H.
; APPLICANT: PAREKH, RAJESH B.
; APPLICANT: POTTER, DAVID M.
; APPLICANT: ROHLFF, CHRISTIAN
; APPLICANT: SILBER, B. MICHAEL
; APPLICANT: SNYDER, PETER J.
; APPLICANT: SOARES, HOLLY D.
; APPLICANT: STIGER, THOMAS R.
; APPLICANT: SUNDERLAND, P. TREY
; APPLICANT: TOWNSEND, ROBERT R.
; APPLICANT: WHITE, W. FROST
; APPLICANT: WILLIAMS, STEPHEN A.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
; TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: POA-002.01
; CURRENT APPLICATION NUMBER: US/10/264,309
; CURRENT FILING DATE: 2002-10-03
; PRIOR APPLICATION NUMBER: 60/326,708
; PRIOR FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 491

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; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 460
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460

Query Match
Best Local Similarity 60.6%; Score 20; DB 15; Length 7;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 10
US-10-601-100-105
; Sequence 105, Application US/10601100
; Publication No. US20040072261A1
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; FILE REFERENCE: 11362.0038 NPUS01
; CURRENT APPLICATION NUMBER: US/10/601,100
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: EP 02447121.1
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/396,437
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105
; LENGTH: 7
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105

Query Match
Best Local Similarity 60.6%; Score 20; DB 15; Length 7;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 11
US-10-700-340-52
; Sequence 52, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BRE
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-154

Query Match
Best Local Similarity 60.6%; Score 20; DB 17; Length 7;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 12
US-10-700-340-154
; Sequence 154, Application US/10700340
; Publication No. US20040203023A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF BRE
; FILE REFERENCE: 2543-1-032
; CURRENT APPLICATION NUMBER: US/10/700,340
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/GB02/02022
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: GB0110790.3
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: GB0118385.4
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: GB0119791.2
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB0120045.0
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: GB0128062.7
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-340-154

Query Match
Best Local Similarity 42.9%; Score 20; DB 17; Length 7;
Matches 3; Conservative 3; Mismatches 3; Indels 1; Gaps 0;

QY 1 FTLKISR 7
Db 1 YTFELSR 7

RESULT 13
US-09-996-288-164
; Sequence 164, Application US/09996288
; Patent No. US20020177128A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxia
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-996-288-164

Query Match      54.5%; Score 18; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKIS 6
       |:|:|
Db      2 TMKLS 6

RESULT 14
US-09-996-265-164
; Sequence 164, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 164
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-164

Query Match      54.5%; Score 18; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 TLKIS 6
       |:|:|
Db      2 TMKLS 6

RESULT 15
US-10-162-497-78
; Sequence 78, Application US/10162497
; Publication No. US20030158398A1
; GENERAL INFORMATION:
; APPLICANT: Chen, H.
; APPLICANT: Freimer, N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
; FILE REFERENCE: 7853-138
; CURRENT APPLICATION NUMBER: US/10/162,497
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US/09/657,474
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 09/268,992
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/236,134
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/106,056
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/088,312
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/078,044
; PRIOR FILING DATE: 1998-03-16
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 78
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-497-78
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Query Match      54.5%; Score 18; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 FTLKIS 6
       |:|:|
Db      2 YTMKYS 7
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Search completed: November 4, 2004, 07:21:29
Job time : 141 secs

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THE USPTO

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 38 Seconds
(without alignments)
12.216 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	32	1	US-08-477-877B-33
2	33	100.0	32	1	US-07-977-696C-71
3	33	100.0	32	1	US-08-129-930B-71
4	33	100.0	32	2	US-08-472-281A-33
5	33	100.0	32	2	US-08-477-989B-33
6	33	100.0	32	3	US-08-976-288A-71
7	33	100.0	32	4	US-08-563-222C-80
8	33	100.0	32	4	US-08-563-222C-114
9	33	100.0	81	1	US-08-497-312-19
10	33	100.0	81	4	US-08-254-180C-154
11	33	100.0	81	4	US-08-254-180C-155
12	33	100.0	81	4	US-08-254-180C-156
13	33	100.0	81	4	US-08-254-180C-157
14	33	100.0	81	4	US-08-254-180C-158
15	33	100.0	81	4	US-08-254-180C-159
16	33	100.0	100	4	US-09-472-087-113
17	33	100.0	100	4	US-09-472-087-115
18	33	100.0	100	4	US-08-840-459-21
19	33	100.0	100	4	US-08-840-459-22
20	33	100.0	100	4	US-08-840-459-23
21	33	100.0	100	4	US-08-840-459-24
22	33	100.0	100	4	US-08-840-459-25
23	33	100.0	100	4	US-08-840-459-26
24	33	100.0	100	4	US-08-840-459-27
25	33	100.0	100	4	US-08-840-459-28
26	33	100.0	100	4	US-08-840-459-29
27	33	100.0	100	4	US-09-840-459-30

Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 37, Appl
Sequence 151, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 151, Appl
Sequence 15, Appl

4 US-09-497-625A-21
4 US-09-497-625A-22
4 US-09-497-625A-23
4 US-09-497-625A-24
4 US-09-497-625A-25
4 US-09-497-625A-26
4 US-09-497-625A-27
4 US-09-497-625A-28
4 US-09-497-625A-29
4 US-09-497-625A-30
3 US-08-881-037-37
1 US-08-488-113B-151
1 US-08-477-484B-151
1 US-08-107-689D-15
1 US-08-472-788A-15
2 US-08-477-531B-15
2 US-08-646-360-151
2 US-08-082-842A-15

ALIGNMENTS

RESULT 1

US-08-477-877B-33
; Sequence 33, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; TITLE OF INVENTION: LO-C2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; US-08-477-877B-33

Query Match 100.0%; Score 33; DB 1; Length 32;

Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0; Mismatches 0;
Matches 7; Conservative 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 2
US-07-977-696C-71
; Sequence 71, Application US/07977696C
; Patent No. 5792852
; GENERAL INFORMATION:
; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESS: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 11-16-92
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38227
; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6688
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-696C-71
Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 3
US-08-129-930B-71
; Sequence 71, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and

; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRPCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-08-129-930B-71
Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 15 FTLKISR 21
RESULT 4
US-08-472-281A-33
; Sequence 33, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latine, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carcella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: 08/407,009
; APPLICATION NUMBER:
; FILING DATE: 29-MAR-1995

APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-472-281A-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 5

US-08-477-989B-33
Sequence 33, Application US/08477989B
Patent No. 5951383

GENERAL INFORMATION:

APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Thereof for Inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 6

US-08-976-288A-71
Sequence 71, Application US/08976288A
Patent No. 6315997

GENERAL INFORMATION:

APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder & Poplawski
STREET: 444 South Flower St., 19th Floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P6639938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-71

Query Match 100.0%; Score 33; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 7
US-09-563-222C-80
; Sequence 80, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-80

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 8
US-09-563-222C-114
; Sequence 114, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-114

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 9
US-08-497-312-19
; Sequence 19, Application US/08497312
; Patent No. 5712120
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method for obtaining modified
; TITLE OF INVENTION: immunoglobulins with reduced immunogenicity of murine
; TITLE OF INVENTION: antibody variable domains, compositions containing them.
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
; STREET: 215 Y 15, ATABEY PLAYA
; CITY: HAVANA
; STATE:
; COUNTRY: CUBA
; ZIP: 11600
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/497,312
; FILING DATE: 30-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CU 80/94
; FILING DATE: 30-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BOND, LAURENCE B.
; REGISTRATION NUMBER: 30,549
; REFERENCE/DOCKET NUMBER: 2629US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 801/532-1922
; TELEFAX: 801/531-9168
; TELEX: 388961 LPMO4UT
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-497-312-19

Query Match 100.0%; Score 33; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 53 FTLKISR 59

RESULT 10
US-09-254-180C-154
; Sequence 154, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, YASUYUKI
; APPLICANT: MAEDA, HIROAKI
; APPLICANT: USHIO, YOSHITAKA
; APPLICANT: HIGUCHI, HIROFUMI
; APPLICANT: NAKATA, MOTOMI
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-154

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 11
US-09-254-180C-155
; Sequence 155, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: OKUMURA, Ko
; APPLICANT: ED, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254.180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-155

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 12
US-09-254-180C-156
; Sequence 156, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: OKUMURA, Ko
; APPLICANT: ED, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi

; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254.180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-156

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 13
US-09-254-180C-157
; Sequence 157, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: ED, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254.180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 157
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-157

Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 FTLKISR 59

RESULT 14
US-09-254-180C-158

```
; Sequence 158, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 158
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-158
```

```
Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 FTLKISR 7
Db 53 FTLKISR 59
```

```
RESULT 15
US-09-254-180C-159
; Sequence 159, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, KO
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 159
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-159
```

```
Query Match 100.0%; Score 33; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4;
```

```
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
Db 53 FTLKISR 59
Search completed: November 4, 2004, 06:53:08
Job time : 39 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 38 Seconds
(without alignments)
17.724 Million cell updates/sec

Title: US-09-712-819D-6
Perfect score: 33
Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	54	2	Ig kappa chain V r
2	33	100.0	71	2	Ig kappa chain V r
3	33	100.0	72	2	Ig kappa chain V r
4	33	100.0	75	2	Ig kappa chain V-J
5	33	100.0	83	2	Ig kappa chain V r
6	33	100.0	83	2	Ig kappa chain V r
7	33	100.0	87	2	Ig kappa chain V r
8	33	100.0	87	2	Ig kappa chain V r
9	33	100.0	89	2	Ig kappa chain V r
10	33	100.0	91	2	Ig kappa chain V r
11	33	100.0	91	2	Ig kappa chain V r
12	33	100.0	93	2	Ig kappa chain V r
13	33	100.0	94	2	Ig kappa chain V r
14	33	100.0	96	2	Ig kappa chain V r
15	33	100.0	99	2	Ig kappa chain V r
16	33	100.0	99	2	Ig kappa chain V r
17	33	100.0	99	2	Ig kappa chain V r
18	33	100.0	100	2	Ig kappa chain V r
19	33	100.0	100	2	Ig kappa chain V r
20	33	100.0	100	2	Ig kappa chain V r
21	33	100.0	101	2	Ig kappa chain V r
22	33	100.0	101	2	Ig kappa chain V r
23	33	100.0	101	2	Ig kappa chain V r
24	33	100.0	102	2	Ig kappa chain V r
25	33	100.0	102	2	Ig kappa chain V r
26	33	100.0	102	2	Ig kappa chain V r
27	33	100.0	102	2	Ig kappa chain V r
28	33	100.0	102	2	Ig kappa chain V r
29	33	100.0	102	2	Ig kappa chain V r

30	33	100.0	102	2	E28195	Ig kappa chain V r
31	33	100.0	102	2	PH1044	Ig kappa chain V r
32	33	100.0	103	2	PH1099	Ig kappa chain V r
33	33	100.0	103	2	PH1056	Ig kappa chain V r
34	33	100.0	103	2	PH1100	Ig kappa chain V r
35	33	100.0	103	2	PH1041	Ig kappa chain V r
36	33	100.0	103	2	PH1098	Ig kappa chain V r
37	33	100.0	103	2	PH1040	Ig kappa chain V r
38	33	100.0	103	2	PH1045	Ig kappa chain V r
39	33	100.0	103	2	PH1042	Ig kappa chain V r
40	33	100.0	103	2	PH1031	Ig kappa chain V r
41	33	100.0	103	2	PH1034	Ig kappa chain V r
42	33	100.0	103	2	PH1038	Ig kappa chain V r
43	33	100.0	103	2	PH1030	Ig kappa chain V r
44	33	100.0	103	2	PH1043	Ig kappa chain V r
45	33	100.0	103	2	PH1055	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S34093
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 07-May-1999
C:Accession: S34093
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A>Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34093
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-54 <WAG>
A:Cross-references: EMBL:X67177
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 FTLKISR 7
Db 43 FTLKISR 49

RESULT 2

H30538
Ig kappa chain V region (174.3F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 09-May-1997
C:Accession: H30538
R:Clafilin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A>Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Accession: H30538
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-71 <CLA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.67; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 1 FTLKISR 7
Db 35 FTLKISR 41

Query Match 100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.77; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 59 FTLKISR 65

RESULT 6
IG kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34095
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: UNIPROT:Q8TCD0; UNIPROT:Q9UL80; EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-80/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.77; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 61 FTLKISR 67

RESULT 7
IG kappa chain V region (patient 19 and 20) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C:Accession: S34091; S34092
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34091
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X67175
A:Experimental source: patient 19
A:Accession: S34092
A:Molecule type: DNA
A:Residues: 1-87 <WAW>
A:Cross-references: EMBL:X67176
A:Experimental source: patient 20
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:3-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.81; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 63 FTLKISR 69

RESULT 8
S34094

Query Match 100.0%; Score 33; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.67; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 28 FTLKISR 34

RESULT 4
S40337
IG kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40337
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40337
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-75 <KLE>
A:Cross-references: EMBL:X72468; NID:g441404; PIDN:CAA51136.1; PID:g441405
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.7; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
DB 30 FTLKISR 36

RESULT 5
S24211
IG kappa chain V region (V3a) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24211
R:Fargent, W.; Meindl, A.; Thiebe, R.; Witzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O region
A:Reference number: S24205; MUID:91330953; PMID:1907917
A:Accession: S24211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <PAR>
A:Cross-references: EMBL:X59317; NID:g33270; PIDN:CAA42004.1; PID:g33271
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34094
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-87 <WAG>
A:Cross-references: UNIPROT:Q9UL80; EMBL:X67178
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/3-82/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 63 FTLKISR 69

RESULT 9
B25155
Ig kappa chain V region (SM1.5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Dec-1987 #sequence_revision 02-Jun-1988 #text_change 16-Aug-1996
C:Accession: B25155
R:Robbins, P.F.; Rosen, E.M.; Haba, S.; Nisonoff, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1050-1054, 1986
A:Title: Relationship of V(H) and V(L) genes encoding three idiotypic families of anti-p
A:Reference number: A94093; MUID:86149212; PMID:3081888
A:Accession: B25155
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-89 <ROB>
C:Comment: This chain is expressed in an IgM with anti-arsenate activity.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 54 FTLKISR 60

RESULT 10
S42186
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S42186; S42195
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42176; MUID:94009207; PMID:7691608
A:Accession: S42186
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <MOJ>
A:Cross-references: EMBL:Z25442; NID:9407830; PIDN:CAA80929.1; PID:9407831
A:Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85 a
A:Accession: S42195
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <MO2>

A:Cross-references: EMBL:Z25460; NID:9407848; PIDN:CAA80947.1; PID:9407849
A:Note: the authors translated the codon GTT for residue 81 as Thr, TGG for residue 85
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F/7-86/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 67 FTLKISR 73

RESULT 11

S25463
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S25463
R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.
submitted to the EMBL Data Library, July 1992
A:Description: Structure and binding properties of monoclonal antibodies to core histon
A:Reference number: S25174
A:Accession: S25463
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-91 <MON>
A:Cross-references: EMBL:X67624; NID:952189; PIDN:CAA47882.1; PID:9938264
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 76 FTLKISR 82

RESULT 12

PH1039
Ig light chain V region (clone 165.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: PH1039
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0971; MUID:92381444; PMID:1512540
A:Accession: PH1039
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-93 <TIL>
A:Cross-references: UNIPROT:Q99M37
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
|||||
Db 67 FTLKISR 73

RESULT 13

PL0258
Ig kappa chain V region (anti-DNA, 1B81VK) - mouse (fragment)

```
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: P10258
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J;Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: P10231; PMID:9011618; PMID:2104919
A;Accession: P10258
A;Molecule type: mRNA
A;Residues: 1-94 <SHL>
A;Cross-references: UNIPROT:Q9JL82
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-6/Region: framework 1
F;7-22/Region: complementarity-determining 1
F;23-37/Region: framework 2
F;38-44/Region: complementarity-determining 2
F;45-76/Region: framework 3
F;77-85/Region: complementarity-determining 3
F;86-94/Region: framework 4

Query Match 100.0%; Score 33; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 59 FTLKISR 65

RESULT 14
S40320
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S40320
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Burr, J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; PMID:9408091; PMID:8258341
A;Accession: S40320
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-96 <KLE>
A;Cross-references: EMBL:X72430; NID:G441328; PIDN:CAA51098.1; PID:G441329
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 33; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 59 FTLKISR 65

RESULT 15
E28833
Ig heavy chain V region (HP22.111.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: E28833
R;Corbet, S.; Hirn, M.; Roth, C.; Theze, J.; Fougereau, M.; Schiff, C.
J. Immunol. 141, 779-784, 1988
A;Title: Allogeic manipulation of the CAT idiotypic cascade. Immunization of C57BL/6 m
A;Reference number: A92827; PMID:88285674; PMID:3135311
A;Accession: E28833
A;Molecule type: mRNA
A;Residues: 1-99 <COR>
A;Cross-references: UNIPROT:Q8VC16
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
```

```
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 33; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 76 FTLKISR 82

Search completed: November 4, 2004, 06:52:23
Job time : 39 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 190 Seconds
(without alignments)
21.198 Million cell updates/sec

Title: US-09-712-819D-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	100.0	86	Q7Z3Y5	Q7Z3Y5 homo sapien
2	33	100.0	102	AAR11040	AAR11040 mus muscu
3	33	100.0	104	Q9JL82	Q9JL82 mus muscu
4	33	100.0	104	AAR11024	AAR11024 mus muscu
5	33	100.0	104	AAR11056	AAR11056 mus muscu
6	33	100.0	104	AAR11063	AAR11063 mus muscu
7	33	100.0	105	AAR11074	AAR11074 mus muscu
8	33	100.0	109	AAR10990	AAR10990 mus muscu
9	33	100.0	112	1 KV2C HUMAN	P01616 homo sapien
10	33	100.0	113	1 KV2D HUMAN	P01617 homo sapien
11	33	100.0	113	1 KV2G MOUSE	P01631 mus muscu
12	33	100.0	114	2 Q9UL30	Q9UL30 mus muscu
13	33	100.0	114	2 AAR11017	Q9UL80 homo sapien
14	33	100.0	115	1 KV2A HUMAN	AAR11017 mus muscu
15	33	100.0	117	1 KV2E HUMAN	P01614 homo sapien
16	33	100.0	133	1 KV2F HUMAN	P06309 homo sapien
17	33	100.0	148	2 Q8K172	P06310 homo sapien
18	33	100.0	238	2 Q9M37	Q8K122 mus muscu
19	33	100.0	238	2 Q8VC16	Q9M37 mus muscu
20	33	100.0	239	2 Q6P491	Q8VC16 mus muscu
21	33	100.0	239	2 Q8K0F8	Q6P491 homo sapien
22	33	100.0	239	2 Q8VC55	Q8K0F8 mus muscu
23	33	100.0	239	2 AAH63599	Q8VC55 mus muscu
24	33	100.0	240	2 Q6PH6	AAH63599 homo sapi
25	33	100.0	240	2 AAH34142	Q6PH6 homo sapien
26	31	93.9	1430	1 UL3C MOUSE	AAH34142 homo sapi
27	30	90.9	99	2 AAR11054	Q8K0T7 mus muscu
28	30	90.9	104	2 AAR11064	AAR11054 mus muscu
29	30	90.9	112	1 KV2D MOUSE	AAR11064 mus muscu
30	30	90.9	112	2 Q6LEM8	P01629 mus muscu
31	30	90.9	112	2 BAD00151	Q6LEM8 mus muscu
					BAD00151 mus muscu

32	30	90.9	113	1 KV2B HUMAN	P01615 homo sapien
33	30	90.9	113	1 KV2E MOUSE	P03976 mus muscu
34	30	90.9	113	1 KV2F MOUSE	P01630 mus muscu
35	30	90.9	135	2 BAC03982	BAC03982 homo sapi
36	30	90.9	239	2 Q8NEK0	Q8NEK0 homo sapien
37	30	90.9	239	2 Q8TCD0	Q8TCD0 homo sapien
38	30	90.9	367	2 Q7MZU1	Q7MZU1 photorhabdu
39	30	90.9	531	1 ANM3 HUMAN	Q60678 homo sapien
40	30	90.9	548	2 Q8WUV3	Q8WUV3 homo sapien
41	30	90.9	588	2 Q7QAX1	Q7QAX1 anopheles g
42	30	90.9	638	2 Q46453	Q46453 clostridium
43	30	90.9	764	2 Q8IKT5	Q8IKT5 plasmodium
44	30	90.9	772	1 C1FB_CLOTM	Q01866 clostridium
45	30	90.9	1853	1 C1FA_CLOTM	Q06851 clostridium

ALIGNMENTS

RESULT 1
Q7Z3Y5 PRELIMINARY; PRT; 86 AA.
ID Q7Z3Y5
AC Q7Z3Y5;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN Name=VKA17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Hogkin lymphoma;
RC Tissue=Hogkin lymphoma;
RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
RA Hansmann M.L., Brauminger A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ564426; CAD92033.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

Query Match 100.0%; Score 33; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 55 FTLKISR 61

RESULT 2
AAR11040 PRELIMINARY; PRT; 102 AA.
ID AAR11040
AC AAR11040;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP TISSUE=Spleen;
RC STRAIN=B6.S1el; LIANG Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;

RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436880; AAR11040.1; -.
 FT NON_TER 1
 FT NON_TER 102
 SQ SEQUENCE 102 AA; 11112 MW; A08600D2B09ABA92 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 DB 74 FTLKISR 80

RESULT 3

Q9JL82 PRELIMINARY; PRT; 104 AA.
 ID Q9JL82
 AC Q9JL82;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Anti-myxin immunoglobulin light chain variable region (Fragment).
 DE Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive with cardiac myosin".
 RL Infect. Immun. 68:5803-5808 (2000).
 DR EMBL; AF206024; AAF69322.1; -.
 DR PIR; P0258; P0258.
 DR PIR; S26334; S26334.
 DR PDB; 1DLF; X-ray.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003396; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11360 MW; 5DA8BFD5FOAIAE CRC64;

Query Match 100.0%; Score 33; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 5.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 DB 68 FTLKISR 74

RESULT 4

AAR11024 PRELIMINARY; PRT; 104 AA.
 ID AAR11024
 AC AAR11024;
 DT 02-MAR-2004 (TREMELrel. 27, Created)
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=B6.Sle1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436864; AAR11024.1; -.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11310 MW; 2CF631F3058E2BB9 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 DB 73 FTLKISR 79

RESULT 5

AAR11056 PRELIMINARY; PRT; 104 AA.
 ID AAR11056
 AC AAR11056;
 DT 02-MAR-2004 (TREMELrel. 27, Created)
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.Sle1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436896; AAR11056.1; -.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11327 MW; BFC116BEF36AB51A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 DB 73 FTLKISR 79

RESULT 6

AAR11063 PRELIMINARY; PRT; 104 AA.
 ID AAR11063
 AC AAR11063;
 DT 02-MAR-2004 (TREMELrel. 27, Created)
 DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
 DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
 DE ANA immunoglobulin kappa light chain (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B6.Sle1; TISSUE=Spleen;
 RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
 RT "Antinuclear autoantibodies from B6.Sle1 mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436903; AAR11063.1; -.
 FT NON_TER 1
 FT NON_TER 104
 SQ SEQUENCE 104 AA; 11304 MW; 9359D08600C6E65A CRC64;

Query Match 100.0%; Score 33; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 5.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 DB 73 FTLKISR 79

```
Query Match      100.0%; Score 33; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 5.5; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 FTLKISR 7
Db 74 FTLKISR 80

RESULT 7
KV2C HUMAN PRELIMINARY; PRT; 105 AA.
AC AAR11074
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436914; AAR11074.1; -.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11378 MW; BCE358D08600CEC0 CRC64;

Query Match      100.0%; Score 33; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 FTLKISR 7
Db 74 FTLKISR 80

RESULT 8
AAR10990 PRELIMINARY; PRT; 109 AA.
AC AAR10990
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DE ANA immunoglobulin kappa light chain (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1e1; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1e1 mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY436830; AAR10990.1; -.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11894 MW; BFA0941FA01908FD CRC64;

Query Match      100.0%; Score 33; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.8; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 FTLKISR 7
Db 68 FTLKISR 74
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RESULT 9
KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HOML.
DR HSP; Q99M37; I191.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 38 Complementarity-determining-1.
FT DOMAIN 39 53 Framework-2.
FT DOMAIN 54 60 Complementarity-determining-2.
FT DOMAIN 61 92 Framework-3.
FT DOMAIN 93 101 Complementarity-determining-3.
FT DOMAIN 102 111 Framework-4.
FT DISULFID 23 92 By similarity.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match      100.0%; Score 33; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 5.9; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 FTLKISR 7
Db 75 FTLKISR 81

RESULT 10
KV2D HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=7414840; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=7316638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Oesserman E.F.,
```

RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RL patient with plasma cell dyscrasia and amyloidosis.";
CC J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: The major amyloid protein appears to be identical
CC with the Bence Jones protein isolated from the same patient.
CC -!- MISCELLANEOUS: This protein was isolated from the urine of a
CC patient with plasma cell dyscrasia and amyloidosis.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
DR PIR; A90370; K2HUTW.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DOMAIN 103 112 By similarity.
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 11
KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 28-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RT anti-digoxin hybridoma antibody."
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma
CC protein that binds digoxin.
DR PIR; A01914; KVM526.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.

FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 100.0%; Score 33; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 12
Q9UL80 PRELIMINARY; PRT; 114 AA.
ID Q9UL80;
AC Q9UL80;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; Q99M37; 1191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER 114 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 100.0%; Score 33; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 76 FTLKISR 82

RESULT 13
AAR11017 PRELIMINARY; PRT; 114 AA.
ID AAR11017;
AC AAR11017;
DT 02-MAR-2004 (TREMELrel. 27, Created)
DT 02-MAR-2004 (TREMELrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMELrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (Fragment).

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=B6.S1el; TISSUE=Spleen;
 RA Liang Z.; Xie C.; Chen C.; Kreska D.; Hsu K.; Zhou J.X.; Mohan C.;
 RT "Antinuclear autoantibodies from B6.S1el mice."
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY436857; AAR11017.1; -
 FT NON_TER 1
 FT NON_TER 114 114
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12422 MW; C94A4DDCF5E8A8C CRC64;

Query Match 100.0%; Score 33; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 |||||
 Db 73 FTLKISR 79

RESULT 14
 ID KV2A HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-II region CUM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN [2]
 RP REVISIONS TO 50; 52; 96 AND 97.
 RX MEDLINE=70063440; PubMed=4188189;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation."
 RL Naturwissenschaften 56:195-205(1969).
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; B91639; K2HUGM.
 DR HSSP; P01751; 1NOB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 4
 FT CHAIN <1 117
 FT DOMAIN 5 27
 FT DOMAIN 28 43
 FT DOMAIN 44 58
 FT DOMAIN 59 65
 FT DOMAIN 66 97
 FT DOMAIN 98 106
 FT DOMAIN 107 116
 FT DISULFID 27 97
 FT NON_TER 117 117
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;
 Query Match 100.0%; Score 33; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 |||||
 Db 73 FTLKISR 79

Query Match 100.0%; Score 33; DB 1; Length 115;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 |||||

Db 78 FTLKISR 84

RESULT 15
 ID KV2E HUMAN STANDARD; PRT; 117 AA.
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region GM607 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191506; PubMed=6325927;
 RA Klobeck H.G.; Solomon A.; Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain diversity.";
 RT Nature 309:73-76(1984).
 CC -----

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 CC -----

EMBL; Z00009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSSP; Q99M37; 1191.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.

FT NON_TER 1 4
 FT SIGNAL <1 117
 FT CHAIN 5 117
 FT DOMAIN 5 27
 FT DOMAIN 28 43
 FT DOMAIN 44 58
 FT DOMAIN 59 65
 FT DOMAIN 66 97
 FT DOMAIN 98 106
 FT DOMAIN 107 116
 FT DISULFID 27 97
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
 Query Match 100.0%; Score 33; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
 |||||
 Db 80 FTLKISR 86

Search completed: November 4, 2004, 06:51:41
 Job time : 193 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:45:39 ; Search time 156 Seconds
(without alignments)
16.097 Million cell updates/sec

Title: US-09-712-819D-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	2 AAW79207	AAW79207 Framework
2	33	100.0	32	4 AAB86295	AAB86295 Murine de
3	33	100.0	32	5 ABP62672	ABP62672 Human imm
4	33	100.0	32	5 ABP62674	ABP62674 Human imm
5	33	100.0	32	5 AAU70400	AAU70400 Human lig
6	33	100.0	32	5 AAU70440	AAU70440 Mouse lig
7	33	100.0	32	7 ADM08541	ADM08541 Canine im
8	33	100.0	32	7 ADM08539	ADM08539 Canine im
9	33	100.0	32	8 ADL93640	ADL93640 Human CD4
10	33	100.0	32	8 ADL93554	ADL93554 Human CD4
11	33	100.0	37	8 ADQ31286	ADQ31286 Humanised
12	33	100.0	50	5 ABG30477	ABG30477 Human ant
13	33	100.0	50	5 ABG30478	ABG30478 Human ant
14	33	100.0	50	5 ABG30479	ABG30479 Human ant
15	33	100.0	81	2 AAR92994	AAR92994 Homologou
16	33	100.0	89	2 AAR80082	AAR80082 Mouse der
17	33	100.0	91	6 ABR55905	ABR55905 Human mAb
18	33	100.0	91	6 ABR55889	ABR55889 Human mAb
19	33	100.0	92	2 AAR27009	AAR27009 Hypercalc
20	33	100.0	93	3 AAY56670	AAY56670 Partial p
21	33	100.0	96	7 ADC99843	ADC99843 Anti-huma
22	33	100.0	96	7 ADD05447	ADD05447 Anti-MUC1
23	33	100.0	96	7 ADF09885	ADF09885 Anti-MUC1
24	33	100.0	99	7 ADK18941	ADK18941 Anti-huma
25	33	100.0	99	7 ADK18899	ADK18899 Anti-huma

ALIGNMENTS

RESULT 1

AAW79207

ID AAW79207 standard; protein; 32 AA.

XX AC AAW79207;

XX XX

DT 21-DEC-1998 (first entry)

XX XX

DE Framework 3 region of human V kappa gene HUM5400.

XX XX

KW Monoclonal antibody; MAb; LO-CD2a; humanised antibody; CD2 antigen;

KW human lymphocyte; immune response; chimeric; graft-versus-host disease;

KW T-cell; transplant rejection; autoimmune disease; HUM5400.

XX XX

OS Homo sapiens.

XX XX

PN US5817311-A.

XX XX

PD 06-OCT-1998.

XX XX

PF 07-JUN-1995; 95US-00472281.

XX XX

PR 05-MAR-1993; 93US-00027008.

PR 09-SEP-1993; 93US-00119032.

PR 29-MAR-1995; 95US-00407009.

XX XX

PA (UYLO-) UNIV CATHOLIQUE LOUVAIN.

XX XX

PI Latine D, Bazin H;

XX XX

PT WPI; 1998-556337/47.

XX XX

PT Inhibition of T-cell mediated immune response with anti-CD2 monoclonal

PT antibody LO-CD2a - used for preventing transplant rejection or for

PT treating graft-versus-host disease or auto-immune diseases.

XX XX

PS Example 7; Col 33-34; 96pp; English.

XX XX

CC This represents the amino acid sequence of the framework 3 region of

CC human V kappa gene HUM5400. This is used to construct a humanised antibody

CC LO-CD2a. The invention relates to the use of the monoclonal antibody

CC (MAb) LO-CD2a or a humanised or a chimeric version of the LO-CD2a

CC antibody for the inhibition of a T-cell mediated immune response in a

CC patient. The MAb LO-CD2a (produced by hybridoma cell line ATCC HB 11423)

CC can bind to an epitope on the CD2 antigen of the human lymphocytes. The T

CC -cell mediated immune response in a patient can be inhibited by

CC administering the MAb LO-CD2a or an antibody that binds to the same human

CC lymphocyte epitope as LO-CD2a. The method is used for preventing

CC

CC

CC

CC

CC

CC

CC

CC

CC transplant rejection or for treating graft-versus-host disease or for
 CC treating autoimmune diseases
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 DB 15 FTLKISR 21
 |||||

RESULT 2
 AAB86295
 ID AAB86295 standard; peptide; 32 AA.
 XX
 AC AAB86295;
 XX
 DT 13-SEP-2001 (first entry)
 XX
 DE Murine derived antibody Wue-1 light chain variable region FW-3.
 XX
 KW Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
 KW immunomodulatory; cognate antigen identification; autoimmune disease;
 KW tumor; multiple myeloma; lymphoma; plasmacytoma; FW-3.
 XX
 OS Mus sp.
 XX
 FN DE19962583-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 23-DEC-1999; 99DE-01062583.
 XX
 PR 23-DEC-1999; 99DE-01062583.
 XX
 PA (MUEL/) MUELLER-HERMELINK H K.
 PA (GREI/) GREINER A.
 XX
 PI Mueller-Hermelink HK, Greiner A;
 XX
 DR WPI; 2001-426596/46.
 XX
 PT New antibodies specific for plasma cells, useful for treatment and
 PT diagnosis of autoimmune diseases and plasma cell tumors.
 XX
 PS Claim 1; Page 10; 18pp; German.
 XX
 CC This invention describes novel antibodies (Ab) in which the variable
 CC region (VR) of at least one chain and/or the VR of at least one heavy
 CC chain includes at least one of 7 specified sequences, or fragments of
 CC these sequences, or contain at least one light chain and/or heavy chain
 CC encoded by specific nucleic acid sequences (i) and (ii), reproduced, or
 CC their fragments. The products of the invention have antitumor and
 CC immunomodulatory activity. Ab, or other antibodies that recognize the
 CC same antigen, are used: (i) to identify cognate antigens; (ii) for
 CC specific labeling of plasma cells (PC), for identification or separation,
 CC e.g. in an extracorporeal system; (iii) for generating additional
 CC antibodies able to label PC; and (iv) for treating autoimmune diseases
 CC and/or tumors, e.g. multiple myeloma, lymphoma and/or plasmacytoma. Ab
 CC are specific for mature PC, i.e. they do not recognize precursor stages,
 CC even though these precursors are used as immunogens. As therapeutic
 CC agents, they should show fewer side effects than conventional
 CC chemotherapeutic agents. This sequence represents the Wue-1 antibody
 CC variable region light chain FW-3 fragment described in the method of the
 CC invention
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 DB 15 FTLKISR 21
 |||||

RESULT 3
 ABP62672
 ID ABP62672 standard; peptide; 32 AA.
 XX
 AC ABP62672;
 XX
 DT 10-OCT-2002 (first entry)
 XX
 DE Human immunopeptide to HCV E2 glycoprotein framework sequence #180.
 XX
 KW Virucide; human; immunopolyptide; immunopeptide; envelope glycoprotein;
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 KW NS3 protein; viral infection.
 XX
 OS Homo sapiens.
 XX
 FN WO200259340-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US002303.
 XX
 PR 26-JAN-2001; 2001US-0264451P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Maruyama T, Jones IM, Burton DR, Fox RI;
 XX
 DR WPI; 2002-599801/64.
 XX
 PT New human immunopolyptide with binding specificity for certain envelope
 PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
 PT diagnosing or treating patients having or suspected of having HCV
 PT infection.
 XX
 PS Claim 4; Fig 17; 308pp; English.
 XX
 CC The present invention relates to human immunopolyptides, produced by a
 CC phage transfected cell library. The present sequence is one such
 CC immunopolyptide. The immunopolyptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolyptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection
 XX
 SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 5; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 DB 15 FTLKISR 21
 |||||

RESULT 4
 ABP62674
 ID ABP62674 standard; peptide; 32 AA.
 XX
 AC ABP62674;
 XX
 DT 10-OCT-2002 (first entry)
 XX

XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds to
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 7
ADM08541
ID ADM08541 standard; peptide; 32 AA.
XX
AC ADM08541;
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 18.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgB; gene therapy; kappa subgenus; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Claim 42; Page 109; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 9
ADL93640
ID ADL93640 standard; peptide; 32 AA.
XX

CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 8
ADM08539
ID ADM08539 standard; peptide; 32 AA.
XX
AC ADM08539;
XX
DT 20-MAY-2004 (first entry)
XX
DE Canine immunoglobulin kappa VL subgenus framework 3 peptide 16.
XX
KW canine; dog; heavy; immunoglobulin; antibody light chain variable domain;
KW antiallergic; allergy; IgB; gene therapy; kappa subgenus; VL framework;
KW FR3.
XX
OS Canis familiaris.
XX
PN WO2003060080-A2.
XX
PD 24-JUL-2003.
XX
PF 20-DEC-2002; 2002WO-US041362.
XX
PR 21-DEC-2001; 2001US-0344874P.
XX
PA (INDEX-) IDEXX LAB INC.
XX
PI Krah ER, Guo H, Aiyappa A, Lawton R;
XX
XX WPI; 2003-598521/56.
XX
PT New canine heavy and light chain variable domain polypeptides, useful for
PT treating canine allergy.
XX
PS Claim 42; Page 109; 130pp; English.
XX
CC The invention relates to a novel canine heavy or light chain variable
CC domain polypeptide. The protein of the invention demonstrates
CC antiallergic activity and may be useful for treating canine allergy,
CC possibly via gene therapy. The current sequence is that of a canine
CC immunoglobulin light chain variable domain framework (FR) peptide of the
CC invention.
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 33; DB 7; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 9
ADL93640
ID ADL93640 standard; peptide; 32 AA.
XX

AC ADL93640;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human CD44-binding antibody FR3-L SEQ ID NO:135.
 XX
 KW human; CD44; light chain immunoglobulin variable domain;
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
 KW antinflammatory; immunosuppressive; antiarthritic; antirheumatic;
 KW dermatological; vasotropic; neuroprotective; antibody therapy;
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
 KW graft versus host response; multiple sclerosis; neoplastic disorder;
 KW cancer; antibody.
 XX
 OS Homo sapiens.
 XX
 FN WO2004024750-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 15-SEP-2003; 2003WO-US029318.
 XX
 PR 13-SEP-2002; 2002US-0410758P.
 XX
 PR 09-MAY-2003; 2003US-0469123P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Rondon IJ, Edge A, Baribault Kent R;
 XX
 XX WPI; 2004-270003/25.
 XX
 PT New protein comprising a light chain (LC) immunoglobulin variable domain
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
 PT useful for preparing a composition for treating inflammatory or
 PT neoplastic disorders.
 XX
 PS Disclosure; SEQ ID NO 135; 128pp; English.
 XX
 CC The invention relates to a novel isolated protein comprising a light
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
 CC immunoglobulin variable domain sequence that form an antigen binding site
 CC with binding affinity for the human CD44 extracellular domain and where
 CC CDR3 of the LC variable domain sequence. A protein of the invention has
 CC cytotstatic, antinflammatory, immunosuppressive, antiarthritic,
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
 CC and may have a use in antibody therapy. The protein is useful for
 CC preparing a composition for treating inflammatory disorders, e.g.,
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or neoplastic disorder, which is a malignant or
 CC metastatic cancer. The present sequence represents a framework (FR)
 CC domain of a human CD44-binding antibody of the invention.
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 33; DB 8; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 DB 15 FTLKISR 21
 RESULT 10
 ID ADL93554
 XX ADL93554 standard; peptide; 32 AA.
 XX
 AC ADL93554;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human CD44-binding antibody H10 VLC FR3 SEQ ID NO:49.
 XX
 KW human; CD44; light chain immunoglobulin variable domain;
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
 KW antinflammatory; immunosuppressive; antiarthritic; antirheumatic;
 KW dermatological; vasotropic; neuroprotective; antibody therapy;
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
 KW graft versus host response; multiple sclerosis; neoplastic disorder;
 KW cancer; antibody.
 XX
 OS Homo sapiens.
 XX
 FN WO2004024750-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 15-SEP-2003; 2003WO-US029318.
 XX
 PR 13-SEP-2002; 2002US-0410758P.
 XX
 PR 09-MAY-2003; 2003US-0469123P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Rondon IJ, Edge A, Baribault Kent R;
 XX
 XX WPI; 2004-270003/25.
 XX
 PT New protein comprising a light chain (LC) immunoglobulin variable domain
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
 PT useful for preparing a composition for treating inflammatory or
 PT neoplastic disorders.
 XX
 PS Disclosure; SEQ ID NO 135; 128pp; English.
 XX
 CC The invention relates to a novel isolated protein comprising a light
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
 CC immunoglobulin variable domain sequence that form an antigen binding site
 CC with binding affinity for the human CD44 extracellular domain and where
 CC CDR3 of the LC variable domain sequence. A protein of the invention has
 CC cytotstatic, antinflammatory, immunosuppressive, antiarthritic,
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
 CC and may have a use in antibody therapy. The protein is useful for
 CC preparing a composition for treating inflammatory disorders, e.g.,
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or neoplastic disorder, which is a malignant or
 CC metastatic cancer. The present sequence represents a framework (FR)
 CC domain of a human CD44-binding antibody of the invention.
 XX
 SQ Sequence 32 AA;
 Query Match 100.0%; Score 33; DB 8; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 DB 15 FTLKISR 21
 RESULT 11
 ID ADQ31286
 XX ADQ31286 standard; peptide; 37 AA.
 XX
 AC ADQ31286;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Humanised murine 1A1 light chain antibody peptide SeqID 52.
 XX
 KW 1A1; monocyte chemotactic protein; beta-chemokine family;
 KW glomerulonephritis; scleroderma; cirrhosis; multiple sclerosis;
 KW lupus nephritis; atherosclerosis; inflammatory bowel disease;
 KW rheumatoid arthritis; inflammatory disease; fibrotic disorder; cancer;
 KW immunopathological disorder; antiarteriosclerotic; antiarthritic;
 KW antinflammatory; antirheumatic; cytotstatic; dermatological;

KW hepatotropic; immunomodulator; nephrotropic; neuroprotective; mouse; MCP;
 KW murine; humanised antibody.
 XX
 OS Mus musculus.
 OS Synthetic.
 XX WO2004050836-A2.
 XX
 XX 17-JUN-2004.
 XX
 XX 25-NOV-2003; 2003WO-US037834.
 XX
 XX 27-NOV-2002; 2002US-0430007P.
 XX
 XX (BIOG-) BIOGEN IDEC MA INC.
 XX
 XX De Fougereolles AR, Kotelianski VE, Garber E, Reid C, Saldanha JW;
 PI Van Vlijmen H;
 XX WPI; 2004-461110/43.
 DR
 XX New antibodies against monocyte chemotactic proteins (MCP), useful for
 PT treating or preventing disorders associated with detrimental MCP
 PT activity, e.g. glomerulonephritis, scleroderma, multiple sclerosis, or
 PT atherosclerosis.
 XX
 PS Disclosure; SEQ ID NO 52; 200pp; English.
 XX
 PS This invention relates to an antibody for treating or preventing
 CC disorders associated with detrimental monocyte chemotactic protein (MCP)
 CC activity. Specifically, it refers to humanised antibodies that bind to
 CC members of the beta-chemokine family (of which MCP-1, MCP-2 and MCP-3
 CC belong) and in particular antibodies that have been modelled on, and
 CC modified from, the variable complementarity determining regions (CDRs) of
 CC the murine 11k2 and 1A1 immunoglobulin sequences. The present invention
 CC describes using these antibodies to treat or prevent diseases and
 CC disorders including glomerulonephritis, scleroderma, cirrhosis, multiple
 CC sclerosis, lupus nephritis, atherosclerosis, inflammatory bowel diseases,
 CC rheumatoid arthritis, inflammatory diseases, fibrotic disorders, cancer
 CC and immunopathological disorders. Accordingly, they can be used in the
 CC development of pharmaceutical compositions that exhibit
 CC antiarteriosclerotic, antiarthritic, antiinflammatory, antirheumatic,
 CC cytostatic, dermatological, hepatotropic, immunomodulatory, nephrotropic
 CC and neuroprotective activities. This peptide sequence is the humanised
 CC murine 1A1 variable and constant light chain antibody peptide of the
 CC invention.
 XX
 SQ Sequence 37 AA;
 Query Match 100.0%; Score 33; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db |||||
 1 FTLKISR 7
 RESULT 12
 ABG30477
 ID ABG30477 standard; protein; 50 AA.
 XX
 AC ABG30477;
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX Human anti-CD40 monoclonal antibody 5H7 light chain #2.
 DE
 XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
 KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
 KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
 KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
 KW proliferation.

XX Homo sapiens.
 OS
 XX WO200228904-A2.
 PN
 XX 11-APR-2002.
 PD
 XX
 XX 02-OCT-2001; 2001WO-US030857.
 PF
 XX 02-OCT-2000; 2000US-0237556P.
 XX
 XX (CHIR) CHIRON CORP.
 PA
 PI Chu K, Wang C, Yoshihara C, Donnelly JJ;
 PI WPI; 2002-405169/43.
 DR
 XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
 PT proliferation, growth or differentiation of a normal human B cells and
 PT treating autoimmune disease such as rheumatoid arthritis or systemic
 PT lupus erythematosus.
 XX
 PS Claim 1; Fig 5; 75pp; English.
 XX
 PS The invention relates to a human monoclonal antibody or fragment capable
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
 CC on the surface of human B cells), where the antibody or fragment is free
 CC of significant agonistic activity, when it binds to the CD40 antigen, and
 CC the growth or differentiation is inhibited. The fragments comprise the
 CC complementarity determining region (CDR) of the light and heavy chains of
 CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
 CC 20C4, 12D9, 9P7 and 13E4. Also included are the nucleic acids encoding
 CC the antibody (or fragments). The antibodies or fragments are used for
 CC inhibiting proliferation, growth or differentiation of a normal human B
 CC cells and to inhibit antibody production by B cells. They may also be
 CC useful for treating autoimmune diseases, such as systemic lupus
 CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
 CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
 CC Hodgkin's Lymphoma). The present sequence represents the antibody 5H7
 CC (another anti-CD40 antibody) light chain
 XX
 SQ Sequence 50 AA;
 Query Match 100.0%; Score 33; DB 5; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db |||||
 15 FTLKISR 21
 RESULT 13
 ABG30478
 ID ABG30478 standard; protein; 50 AA.
 XX
 AC ABG30478;
 XX
 XX 07-OCT-2002 (first entry)
 DT
 XX Human anti-CD40 monoclonal antibody 9F7 light chain #2.
 DE
 XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
 KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
 KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
 KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
 KW proliferation.
 XX
 OS Homo sapiens.
 XX WO200228904-A2.
 PN
 XX 11-APR-2002.

XX 02-OCT-2001; 2001WO-US030857.
 XX
 XX 02-OCT-2000; 2000US-0237556P.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
 XX WPI; 2002-405169/43.
 XX
 XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
 PT proliferation, growth or differentiation of a normal human B cells and
 PT treating autoimmune disease such as rheumatoid arthritis or systemic
 PT lupus erythematosus.
 XX
 XX Claim 1; Fig 5; 75pp; English.
 XX
 XX The invention relates to a human monoclonal antibody or fragment capable
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
 CC on the surface of human B cells), where the antibody or fragment is free
 CC of significant agonistic activity when it binds to the CD40 antigen, and
 CC the growth or differentiation is inhibited. The fragments comprise the
 CC complementarity determining region (CDR) of the light and heavy chains of
 CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
 CC 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
 CC the antibody (or fragments). The antibodies or fragments are used for
 CC inhibiting proliferation, growth or differentiation of a normal human B
 CC cells and to inhibit antibody production by B cells. They may also be
 CC useful for treating autoimmune diseases, such as systemic lupus
 CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
 CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
 CC Hodgkin's lymphoma). The present sequence represents the antibody 9F7
 CC light chain
 XX
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 33; DB 5; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db 15 FTLKISR 21
 RESULT 14
 ABG30479
 ID ABG30479 standard; protein; 50 AA.
 XX
 XX ABG30479;
 AC
 XX 07-OCT-2002 (first entry)
 DT
 DE Human anti-CD40 monoclonal antibody 15B8 light chain #2.
 XX
 XX Human; light chain; CD40; autoimmune disease; multiple sclerosis;
 KW systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
 KW Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
 KW non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
 KW proliferation.
 XX
 XX Homo sapiens.
 OS
 XX WO200228904-A2.
 XX
 XX 11-APR-2002.
 PD
 XX 02-OCT-2001; 2001WO-US030857.
 XX
 XX 02-OCT-2000; 2000US-0237556P.
 XX
 XX (CHIR) CHIRON CORP.
 PA

XX Chu K, Wang C, Yoshihara C, Donnelly JJ;
 XX WPI; 2002-405169/43.
 XX
 XX A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
 PT proliferation, growth or differentiation of a normal human B cells and
 PT treating autoimmune disease such as rheumatoid arthritis or systemic
 PT lupus erythematosus.
 XX
 XX Claim 1; Fig 5; 75pp; English.
 XX
 XX The invention relates to a human monoclonal antibody or fragment capable
 CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
 CC on the surface of human B cells), where the antibody or fragment is free
 CC of significant agonistic activity when it binds to the CD40 antigen, and
 CC the growth or differentiation is inhibited. The fragments comprise the
 CC complementarity determining region (CDR) of the light and heavy chains of
 CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
 CC 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
 CC the antibody (or fragments). The antibodies or fragments are used for
 CC inhibiting proliferation, growth or differentiation of a normal human B
 CC cells and to inhibit antibody production by B cells. They may also be
 CC useful for treating autoimmune diseases, such as systemic lupus
 CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
 CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
 CC Hodgkin's lymphoma). The present sequence represents the antibody 15B8
 CC light chain
 XX
 XX Sequence 50 AA;
 SQ
 Query Match 100.0%; Score 33; DB 5; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLKISR 7
 Db 15 FTLKISR 21
 RESULT 15
 AAR92994
 ID AAR92994 standard; protein; 81 AA.
 XX
 XX AAR92994;
 AC
 XX 25-MAR-2003 (revised)
 DT 18-MAY-1996 (first entry)
 DE
 DE Homologous sequences to antibody IOR-R3 variable region light chain.
 XX
 XX IOR-R3; monoclonal antibody; human; mouse; light chain; homology;
 KW variable region; epidermal growth factor receptor; hybridoma; framework;
 KW cloning; computer; algorithm; immunogenicity; site-directed mutagenesis;
 KW T-lymphocyte epitope; tertiary structure; point mutation;
 KW antibody engineering; protein engineering; humanised antibody;
 KW antitumour; cancer; therapy.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Region 2
 FT /note= "Amino acid involved in tertiary structure"
 FT Region 4
 FT /note= "Amino acid involved in tertiary structure"
 FT Region 24..25
 FT /note= "Amino acids involved in tertiary structure"
 FT Region 35..39
 FT /note= "Amino acids involved in tertiary structure"
 FT Region 46
 FT /note= "Amino acid involved in tertiary structure"
 FT Region 48
 FT /note= "Amino acid involved in tertiary structure"

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OM protein - protein search, using sw model

Run on: November 4, 2004, 06:51:47 ; Search time 142 Seconds
(without alignments)
17.413 Million cell updates/sec

Title: US-09-712-819d-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1566620 seqs, 353225886 residues

Total number of hits satisfying chosen parameters: 1566620

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US10H_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	32	10	US-09-563-222-80
2	33	100.0	32	10	US-09-563-222-120
3	33	100.0	32	10	US-09-947-839-71
4	33	100.0	32	14	US-10-168-809-5
5	33	100.0	32	16	US-10-663-244-49
6	33	100.0	32	16	US-10-663-244-135
7	33	100.0	32	16	US-10-327-598-385
8	33	100.0	32	16	US-10-327-598-389
9	33	100.0	32	17	US-10-783-950-80
10	33	100.0	32	17	US-10-783-950-114
11	33	100.0	93	9	US-09-305-243-61
12	33	100.0	99	14	US-10-041-860-281
13	33	100.0	99	14	US-10-041-860-323

14	33	100.0	99	14	US-10-041-860-365	Sequence 365, App
15	33	100.0	99	14	US-10-308-817-176	Sequence 176, App
16	33	100.0	99	15	US-10-453-698-176	Sequence 176, App
17	33	100.0	100	9	US-09-822-698A-19	Sequence 19, Appl
18	33	100.0	100	9	US-09-840-459-21	Sequence 21, Appl
19	33	100.0	100	9	US-09-840-459-22	Sequence 22, Appl
20	33	100.0	100	9	US-09-840-459-23	Sequence 23, Appl
21	33	100.0	100	9	US-09-840-459-24	Sequence 24, Appl
22	33	100.0	100	9	US-09-840-459-25	Sequence 25, Appl
23	33	100.0	100	9	US-09-840-459-26	Sequence 26, Appl
24	33	100.0	100	9	US-09-840-459-27	Sequence 27, Appl
25	33	100.0	100	9	US-09-840-459-28	Sequence 28, Appl
26	33	100.0	100	9	US-09-840-459-29	Sequence 29, Appl
27	33	100.0	100	9	US-09-840-459-30	Sequence 30, Appl
28	33	100.0	100	14	US-10-194-975-75	Sequence 75, Appl
29	33	100.0	100	14	US-10-194-975-76	Sequence 76, Appl
30	33	100.0	100	14	US-10-194-975-77	Sequence 77, Appl
31	33	100.0	100	14	US-10-194-975-78	Sequence 78, Appl
32	33	100.0	100	14	US-10-194-975-79	Sequence 79, Appl
33	33	100.0	100	14	US-10-194-975-80	Sequence 80, Appl
34	33	100.0	100	14	US-10-194-975-81	Sequence 81, Appl
35	33	100.0	100	14	US-10-125-687-24	Sequence 24, Appl
36	33	100.0	100	14	US-10-153-382-36	Sequence 36, Appl
37	33	100.0	100	14	US-10-153-382-38	Sequence 38, Appl
38	33	100.0	100	14	US-10-041-860-8	Sequence 8, Appli
39	33	100.0	100	14	US-10-041-860-280	Sequence 280, App
40	33	100.0	100	14	US-10-041-860-321	Sequence 321, App
41	33	100.0	100	14	US-10-041-860-364	Sequence 364, App
42	33	100.0	100	14	US-10-010-942B-7	Sequence 7, Appli
43	33	100.0	100	14	US-10-308-817-22	Sequence 22, Appl
44	33	100.0	100	14	US-10-308-817-23	Sequence 23, Appl
45	33	100.0	100	14	US-10-308-817-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-563-222-80
; Sequence 80, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563.222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-80

Query Match 100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 2
US-09-563-222-120
; Sequence 120, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.

; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-120

Query Match 100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 3

US-09-947-839-71
; Sequence 71, Application US/09947839
; Publication No. US20030138428A1
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; Ceriani Dr., Roberto L.
; Peterson Dr., Jerry A.
; Padian Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; Carcinoma Specificity, and Kit and
; Diagnostic Vaccination and
; Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,839
; FILING DATE: 06-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/976,288
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/977,696
; FILING DATE: NO. US20030138428A1ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 71:

US-09-947-839-71

Query Match 100.0%; Score 33; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 4

US-10-168-809-5
; Sequence 5, Application US/10168809
; Publication No. US20030180799A1
; GENERAL INFORMATION:
; APPLICANT: Muller-Hermelink, Hans Konrad
; APPLICANT: GREINER, AXEL
; APPLICANT: DORKEN, BERND
; APPLICANT: BARGOU, RALF
; APPLICANT: KUFER, PETER
; TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS
; FILE REFERENCE: 009848-0272298
; CURRENT APPLICATION NUMBER: US/10/168,809
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/EP00/13238
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: DE 199 62 583.2
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no
; OTHER INFORMATION: natural origin
US-10-168-809-5

Query Match 100.0%; Score 33; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 15 FTLKISR 21

RESULT 5

US-10-663-244-49
; Sequence 49, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-49


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Query Match      100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 15 FTLKISR 21

RESULT 6
US-10-663-244-135
; Sequence 135, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-135

Query Match      100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 15 FTLKISR 21

RESULT 7
US-10-327-598-385
; Sequence 385, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 385
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: X is Y, H, F, or C
US-10-327-598-385
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Query Match      100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 15 FTLKISR 21

RESULT 8
US-10-327-598-389
; Sequence 389, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 389
; LENGTH: 32
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-389

Query Match      100.0%; Score 33; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
   |||||
Db 15 FTLKISR 21

RESULT 9
US-10-783-950-80
; Sequence 80, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/05/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-80

Query Match      100.0%; Score 33; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
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Db 15 FTLKISR 21
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RESULT 10
US-10-783-950-114
; Sequence 114, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-114

Query Match 100.0%; Score 33; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 6.1; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLKISR 7
|||||

RESULT 11
US-09-905-243-61
; Sequence 61, Application US/09905243
; Patent No. US20020062009A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
; FILE REFERENCE: P50770
; CURRENT APPLICATION NUMBER: US/09/905,243
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/300,970
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Macaca cynomolgus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDRI
; NAME/KEY: DOMAIN
; LOCATION: (54)...(61)
; OTHER INFORMATION: CDRII
US-09-905-243-61

Query Match 100.0%; Score 33; DB 9; Length 93;
Best Local Similarity 100.0%; Pred. No. 17; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLKISR 7
|||||

Db 76 FTLKISR 82

RESULT 12
US-10-041-860-281
; Sequence 281, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 31
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 31
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-281

Query Match 100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 18; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLKISR 7
|||||

RESULT 13
US-10-041-860-323
; Sequence 323, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-323

Query Match 100.0%; Score 33; DB 14; Length 99;

Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 76 FTLKISR 82

Qy 1 FTLKISR 7
Db 66 FTLKISR 72

Search completed: November 4, 2004, 07:03:46
Job time : 143 secs

RESULT 14
US-10-041-860-365
; Sequence 365, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFR AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-365

Query Match 100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 76 FTLKISR 82

RESULT 15
US-10-308-817-176
; Sequence 176, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1687-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-308-817-176

Query Match 100.0%; Score 33; DB 14; Length 99;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:51 ; Search time 23.6667 Seconds
(without alignments)
19.615 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	62.5	7	4	US-08-753-750B-20
2	18	56.2	7	3	US-09-187-859-637
3	18	56.2	7	4	US-09-839-542B-637
4	17	53.1	5	3	US-08-757-177-16
5	17	53.1	6	4	US-09-155-613A-59
6	17	53.1	6	4	US-09-266-805-5
7	17	53.1	6	4	US-09-530-139-14
8	17	53.1	7	2	US-08-739-401A-6
9	17	53.1	7	4	US-08-753-750B-19
10	16	50.0	4	3	US-08-860-904-9
11	16	50.0	4	4	US-09-301-593-47
12	16	50.0	6	1	US-08-252-995D-7
13	16	50.0	6	2	US-08-478-386A-46
14	16	50.0	6	2	US-08-292-597-46
15	16	50.0	6	2	US-08-388-653-46
16	16	50.0	6	2	US-08-473-985-46
17	16	50.0	6	2	US-08-834-108-7
18	16	50.0	6	2	US-08-483-898-46
19	16	50.0	6	3	US-08-087-716-46
20	16	50.0	6	3	US-09-157-753-46
21	16	50.0	6	3	US-09-157-230-46
22	16	50.0	6	3	US-09-087-811-46
23	16	50.0	6	3	US-09-156-855-46
24	16	50.0	6	3	US-09-188-010-46
25	16	50.0	6	3	US-09-087-647-46
26	16	50.0	6	3	US-09-302-629-46
27	16	50.0	7	1	US-08-136-743B-55

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28      16      50.0      7      2      US-08-177-109A-7      Sequence 7, Appli
29      16      50.0      7      2      US-08-687-706-7      Sequence 7, Appli
30      16      50.0      7      3      US-09-040-216-28      Sequence 28, Appl
31      15      46.9      5      1      US-08-136-743B-63      Sequence 63, Appl
32      15      46.9      5      2      US-08-667-001-22      Sequence 22, Appl
33      15      46.9      5      3      US-09-040-216-55      Sequence 55, Appl
34      15      46.9      5      3      US-08-591-632-17      Sequence 17, Appl
35      15      46.9      5      3      US-08-591-632-23      Sequence 23, Appl
36      15      46.9      5      3      US-08-591-632-26      Sequence 26, Appl
37      15      46.9      5      3      US-09-611-451-17      Sequence 17, Appl
38      15      46.9      5      3      US-09-611-451-23      Sequence 23, Appl
39      15      46.9      5      3      US-09-611-451-26      Sequence 26, Appl
40      15      46.9      6      1      US-08-136-743B-62      Sequence 62, Appl
41      15      46.9      6      1      US-08-297-731-4       Sequence 4, Appli
42      15      46.9      6      1      US-08-290-448A-41      Sequence 41, Appl
43      15      46.9      6      1      US-08-290-448A-41      Sequence 41, Appl
44      15      46.9      6      1      US-08-175-069A-41      Sequence 41, Appl
45      15      46.9      6      2      US-08-622-720A-8       Sequence 8, Appli

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ALIGNMENTS

RESULT 1

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US-08-753-750B-20
; Sequence 20, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-08-753-750B-20

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Query Match      62.5%      Score 20; DB 4; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 FTLTSS 7
Db      1 FTLSDA 7

```

RESULT 2

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US-09-187-859-637
; Sequence 637, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7

```

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-637

Query Match      56.2%; Score 18; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      ||: ||
Db      1 FTIDSS 7

RESULT 3
US-09-839-542B-637
; Sequence 637, Application US/09839542B
; Patent No. 6569996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407D1
; CURRENT APPLICATION NUMBER: US/09/839,542B
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 637
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-839-542B-637

Query Match      56.2%; Score 18; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 FTLTSS 7
      ||: ||
Db      1 FTIDSS 7

RESULT 4
US-08-757-177-16
; Sequence 16, Application US/08757177
; Patent No. 6071718
; GENERAL INFORMATION:
; APPLICANT: MURKJI, PRADIP
; APPLICANT: HARDS, ROBERT G.
; APPLICANT: THURMOND, JENNIFER M.
; APPLICANT: LEONARD, AMANDA EUN-YEONG
; TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: One Abbott Park Road
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,177
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6004.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 848-938-2623
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-757-177-16

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Query Match      53.1%; Score 17; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TISS 7
      ||||
Db      2 TISS 5

```

```

RESULT 5
US-09-155-613A-59
; Sequence 59, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karavan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-09-155-613A-59

```

```

Query Match      53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 FTILT 4
      :|||
Db      3 YILT 6

```

```

RESULT 6
US-09-266-805-5
; Sequence 5, Application US/09266805
; Patent No. 6517829
; GENERAL INFORMATION:
; APPLICANT: Unilever N.V.

```

```
; APPLICANT: Unilever PLC
; TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
; FILE REFERENCE: t-7055
; CURRENT APPLICATION NUMBER: US/09/266,805
; CURRENT FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: llama
US-09-266-805-5

Query Match          53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LTISS 7
   :|||
Db 2 VTVSS 6

RESULT 7
US-09-530-139-14
; Sequence 14, Application US/09530139
; Patent No. 6670453
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOGT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-530-139-14

Query Match          53.1%; Score 17; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LTISS 7
   :|||
Db 2 VTVSS 6

RESULT 8
US-08-739-401A-6
; Sequence 6, Application US/08739401A
; Patent No. 5837461
; GENERAL INFORMATION:
; APPLICANT: Neitz, Maureen E.
; APPLICANT: Neitz, John F.
; TITLE OF INVENTION: DETECTION OF CONE-PHOTORECEPTOR-BASED
; TITLE OF INVENTION: VISION DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
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; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,401A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 650053.91151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-739-401A-6

Query Match          53.1%; Score 17; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLT 4
   |||
Db 2 FTVT 5

RESULT 9
US-08-753-750B-19
; Sequence 19, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-19

Query Match          53.1%; Score 17; DB 4; Length 7;
Best Local Similarity 33.3%; Pred. No. 3.8e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLTISS 7
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Db 2 TITVTA 7

RESULT 10
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US-08-860-904-9
; Sequence 9, Application US/08860904
; Patent No. 6294654
; GENERAL INFORMATION:
; APPLICANT: Sandlie, Inger
; APPLICANT: Bogen, Bjarne
; APPLICANT: Fossum, Sigbjorn
; TITLE OF INVENTION: A Modified Immunoglobulin Molecule
; TITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR
; TITLE OF INVENTION: Loop Region
; FILE REFERENCE: 9914-1
; CURRENT APPLICATION NUMBER: US/08/860,904
; CURRENT FILING DATE: 1997-09-29
; EARLIER APPLICATION NUMBER: PCT/GB96/00116
; EARLIER FILING DATE: 1996-01-19
; EARLIER APPLICATION NUMBER: GB 9501079.9
; EARLIER FILING DATE: 1995-01-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mus sp.
US-08-860-904-9

Query Match 50.0%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
DB 1 TVSS 4

RESULT 11
US-09-301-593-47
; Sequence 47, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-47

Query Match 50.0%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TISS 7
DB 1 TVSS 4

RESULT 12
US-08-252-995D-7
; Sequence 7, Application US/08252995D

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; Patent No. 5650501
; GENERAL INFORMATION:
; APPLICANT: Dennis, James W
; APPLICANT: Heffernan, Mike
; APPLICANT: Fode, Carol
; TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,995D
; FILING DATE: 02-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Kurdydyk, Linda M
; REGISTRATION NUMBER: 34,971
; REFERENCE/DOCKET NUMBER: 3153-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-252-995D-7

Query Match 50.0%; Score 16; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
DB 2 LTLISN 6

RESULT 13
US-08-478-386A-46
; Sequence 46, Application US/08478386A
; Patent No. 5830462
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,386A
; FILING DATE: 07/JUN/1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-386A-46

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 3 LTIS 6
Db 3 LTVS 6

RESULT 14
US-08-292-597-46
; Sequence 46, Application US/08292597
; Patent No. 5834266
; GENERAL INFORMATION:
; APPLICANT: Gerald R. Crabtree
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: Regulated Apoptosis
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,597
; FILING DATE: 18/AUG/1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-108A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; US-08-292-597-46

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 3 LTIS 6
Db 3 LTVS 6

RESULT 15
US-08-388-653-46
; Sequence 46, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Schreiber, Stuart L.
; APPLICANT: Spencer, David M.
; APPLICANT: Wandless, Thomas J.
; APPLICANT: Belshaw, Peter
; TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/DOS/MS/DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,653
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,386
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Figg, E. Anthony
; REGISTRATION NUMBER: 27,195
; REFERENCE/DOCKET NUMBER: 2054-114A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-388-653-46

Query Match 50.0%; Score 16; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 3 LTIS 6
Db 3 LTVS 6
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 01:23:27 ; Search time 69.3333 seconds
(without alignments)
32.733 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 PTLRISS 7

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Searched: 1370721 seqs, 324215800 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	68.8	6	14	US-10-150-654A-18
2	18	56.2	7	14	US-10-006-869-637
3	18	56.2	7	14	US-10-349-507-11
4	18	56.2	7	14	US-10-267-565-11
5	18	56.2	7	14	US-10-395-032-637
6	17	53.1	5	10	US-09-788-006-107
7	17	53.1	5	10	US-09-788-006-108
8	17	53.1	5	14	US-10-154-971-29
9	17	53.1	5	16	US-10-803-622-2
10	17	53.1	5	16	US-10-803-653-2
11	17	53.1	6	9	US-09-777-921A-17
12	17	53.1	6	10	US-09-530-139-14
13	17	53.1	6	13	US-10-156-820-59
14	22	68.8	6	14	US-10-150-654A-18
15	18	56.2	7	14	US-10-006-869-637
16	18	56.2	7	14	US-10-349-507-11
17	18	56.2	7	14	US-10-267-565-11
18	18	56.2	7	14	US-10-395-032-637
19	17	53.1	5	10	US-09-788-006-107
20	17	53.1	5	10	US-09-788-006-108
21	17	53.1	5	14	US-10-154-971-29
22	17	53.1	5	16	US-10-803-622-2
23	17	53.1	5	16	US-10-803-653-2
24	17	53.1	6	9	US-09-777-921A-17
25	17	53.1	6	10	US-09-530-139-14
26	17	53.1	6	13	US-10-156-820-59

14	17	53.1	6	14	US-10-097-175-97	Sequence 97, Appl
15	17	53.1	6	15	US-10-698-489-17	Sequence 17, Appl
16	16	50.0	4	14	US-09-301-593-47	Sequence 47, Appl
17	16	50.0	4	9	US-10-159-006-47	Sequence 47, Appl
18	16	50.0	6	14	US-10-020-354-102	Sequence 102, Appl
19	16	50.0	6	15	US-10-054-712-46	Sequence 46, Appl
20	16	50.0	6	17	US-10-699-088-519	Sequence 519, Appl
21	16	50.0	7	9	US-09-832-723-69	Sequence 69, Appl
22	16	50.0	7	9	US-09-996-288-164	Sequence 164, Appl
23	16	50.0	7	10	US-09-996-265-164	Sequence 164, Appl
24	16	50.0	7	14	US-10-303-331-69	Sequence 69, Appl
25	16	50.0	7	14	US-10-022-066-214	Sequence 214, Appl
26	16	50.0	7	15	US-10-481-863-164	Sequence 164, Appl
27	15	46.9	5	14	US-10-286-186-3	Sequence 3, Appl
28	15	46.9	5	14	US-10-286-186-4	Sequence 394, Appl
29	15	46.9	5	14	US-10-315-964A-394	Sequence 394, Appl
30	15	46.9	5	14	US-10-317-251A-394	Sequence 394, Appl
31	15	46.9	5	14	US-10-317-252A-394	Sequence 394, Appl
32	15	46.9	6	9	US-09-876-388-6	Sequence 6, Appl
33	15	46.9	6	14	US-10-105-330-39	Sequence 39, Appl
34	15	46.9	6	14	US-10-006-869-650	Sequence 650, Appl
35	15	46.9	6	14	US-10-287-892-6	Sequence 6, Appl
36	15	46.9	6	14	US-10-288-340-6	Sequence 6, Appl
37	15	46.9	6	14	US-10-315-964A-402	Sequence 402, Appl
38	15	46.9	6	14	US-10-317-251A-402	Sequence 402, Appl
39	15	46.9	6	14	US-10-317-252A-402	Sequence 402, Appl
40	15	46.9	6	14	US-10-395-032-650	Sequence 650, Appl
41	15	46.9	6	15	US-10-394-980-243	Sequence 243, Appl
42	15	46.9	6	15	US-10-418-972-55	Sequence 55, Appl
43	15	46.9	6	15	US-10-374-466-47	Sequence 47, Appl
44	15	46.9	6	15	US-10-722-733-6	Sequence 6, Appl
45	15	46.9	6	16	US-10-723-099-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-10-150-654A-18
; Sequence 18, Application US/10150654A
; Publication No. US20030198595A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; APPLICANT: LEUNG, SHUI-ON
; APPLICANT: MCBRIDE, WILLIAM J.
; APPLICANT: QU, ZHENGXING
; TITLE OF INVENTION: PRODUCTION AND USE OF NOVEL PEPTIDE-BASED AGENTS FOR
; FILE REFERENCE: 018733-1085
; CURRENT APPLICATION NUMBER: US/10/150.654A
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/382,186
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 09/823,746
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-150-654A-18

Query Match 68.8%; Score 22; DB 14; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTASS 7
|:|:|

Db 1 TTVSS 6

RESULT 2

US-10-006-869-637

; Sequence 637, Application US/10006869

; Publication No. US20030082166A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C7

; CURRENT APPLICATION NUMBER: US/10/006,869

; CURRENT FILING DATE: 2001-12-03

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 637

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative linear modulating agent based on

; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion

; OTHER INFORMATION: recognition sequence

US-10-006-869-637

Query Match 56.2%; Score 18; DB 14; Length 7;

Best Local Similarity 57.1%; Pred. No. 1.2e+06;

Mismatches 1; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 1;

QY 1 FTITSS 7

Db 1 FTIDSS 7

RESULT 3

US-10-349-507-11

; Sequence 11, Application US/10349507

; Publication No. US20030199002A1

; GENERAL INFORMATION:

; APPLICANT: Hekimi, Siegfried

; APPLICANT: Jiang, Ning

; APPLICANT: Benard, Claire

; APPLICANT: Kebir, Hania

; APPLICANT: McCright, Brenton

; APPLICANT: Lakowski, Bernard

; TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF

; FILE REFERENCE: 11202-006-999

; CURRENT APPLICATION NUMBER: US/10/349,507

; CURRENT FILING DATE: 2003-01-22

; PRIOR FILING DATE: 2003-01-22

; PRIOR FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: PCT/CA01/00913

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: 60/213,174

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/254,932

; PRIOR FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 11

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-349-507-11

Query Match 56.2%; Score 18; DB 14; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0;

QY 2 TLTI 5

Db 1 TLTI 4

RESULT 4

US-10-267-565-11

; Sequence 11, Application US/10267565

; Publication No. US20030204059A1

; GENERAL INFORMATION:

; APPLICANT: Gately, Maurice

; APPLICANT: Gubler, Ulrich

; APPLICANT: Hulmes, Jeffery

; APPLICANT: Podlaski, Frank

; APPLICANT: Stern, Alvin

; TITLE OF INVENTION: PURIFICATION AND CHARACTERIZATION OF CYTOTOXIC

; TITLE OF INVENTION: LYMPHOCTE MATURATION FACTOR AND MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES THERETO

; FILE REFERENCE: 11126-005

; CURRENT APPLICATION NUMBER: US/10/267,565

; CURRENT FILING DATE: 2003-01-23

; PRIOR APPLICATION NUMBER: 09/401,839

; PRIOR FILING DATE: 1999-09-22

; PRIOR APPLICATION NUMBER: 08/459,151

; PRIOR FILING DATE: 1995-06-02

; PRIOR APPLICATION NUMBER: 08/205,011

; PRIOR FILING DATE: 1994-03-02

; PRIOR APPLICATION NUMBER: 07/857,023

; PRIOR FILING DATE: 1992-03-24

; PRIOR APPLICATION NUMBER: 07/572,284

; PRIOR FILING DATE: 1990-08-27

; PRIOR APPLICATION NUMBER: 07/520,935

; PRIOR FILING DATE: 1990-05-09

; PRIOR APPLICATION NUMBER: 07/455,708

; PRIOR FILING DATE: 1989-12-22

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 11

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-267-565-11

Query Match 56.2%; Score 18; DB 14; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;

Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0;

QY 2 TLTI 5

Db 1 TLTI 4

RESULT 5

US-10-395-032-637

; Sequence 637, Application US/10395032

; Publication No. US20030229199A1

; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.

; APPLICANT: Symonds, James Matthew

; APPLICANT: Gour, Barbara J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

; FILE REFERENCE: 100086.407C9

; CURRENT APPLICATION NUMBER: US/10/395,032

; CURRENT FILING DATE: 2003-03-21

; NUMBER OF SEQ ID NOS: 4052

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 637

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Representative linear modulating agent based on

; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion

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; OTHER INFORMATION: recognition sequence
US-10-395-032-637

Query Match          56.2%; Score 18; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 1 FTIDSS 7

RESULT 6
US-09-788-006-107
; Sequence 107, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107

Query Match          53.1%; Score 17; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLT 4
Db 2 FTVT 5

RESULT 7
US-09-788-006-108
; Sequence 108, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE OF INVENTION: Polypeptide Tertiary Structures
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-108

Query Match          53.1%; Score 17; DB 10; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLT 4
Db 1 FTVT 4

RESULT 8
US-10-154-971-29
; Sequence 29, Application US/10154971
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; Publication No. US2003008074A1
; GENERAL INFORMATION:
; APPLICANT: Hamers, Raymond
; APPLICANT: Muyldermans, Serge
; TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
; USE FOR THERAPEUTIC OR VETERINARY PURPOSES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENCER & FRANK
; STREET: 1100 New York Avenue, N.W., Suite 300 East
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/154,971
; FILING DATE: 28-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,244
; FILING DATE: <Unknown>
; APPLICATION NUMBER: PCT/EP96/01725
; FILING DATE: 25-APR-1996
; APPLICATION NUMBER: EP 95400932.0
; FILING DATE: 25-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gollin, Michael A.
; REGISTRATION NUMBER: 31,957
; REFERENCE/DOCKET NUMBER: GUELA 0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-414-4000
; TELEFAX: 202-414-4040
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-154-971-29

Query Match          53.1%; Score 17; DB 14; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LTISS 7
Db 1 VTVSS 5

RESULT 9
US-10-803-622-2
; Sequence 2, Application US/10803622
; Publication No. US20040157214A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
```

```

; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,622
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacteriophage fd
US-10-803-622-2

Query Match 53.1%; Score 17; DB 16; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 1 VTSS 5

RESULT 10
US-10-803-653-2
; Sequence 2, Application US/10803653
; Publication No. US20040157215A1
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clarkson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 13839-00013
; CURRENT APPLICATION NUMBER: US/10/803,653
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Bacteriophage fd
US-10-803-622-2

Query Match 53.1%; Score 17; DB 16; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
Db 1 VTSS 5

RESULT 11
US-09-777-921A-17
; Sequence 17, Application US/09777921A
; Patent No. US20020115136A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921A-17

Query Match 53.1%; Score 17; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 6
Db 2 LTISS 5

RESULT 12
US-09-530-139-14
; Sequence 14, Application US/09530139
; Publication No. US20030092892A1
; GENERAL INFORMATION:
; APPLICANT: FRENKEN, LEON GERARDUS
; APPLICANT: HOWELL, STEVEN
; APPLICANT: LEDEBOER, ADRIANUS MARINUS
; APPLICANT: VAN DER LOOT, CORNELIS PAUL
; TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
; FILE REFERENCE: 60113/268075/ASH
; CURRENT APPLICATION NUMBER: US/09/530,139
; CURRENT FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/EP98/06991
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: EP 97308538.4
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; PRIOR FILING DATE: 1997-10-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-530-139-14

Query Match 53.1%; Score 17; DB 10; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
:||||
Db 2 VIVSS 6

RESULT 13
US-10-156-820-59
; Sequence 59, Application US/10156820
; Publication No. US20020150558A1
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; APPLICANT: Hong, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/10/156.820
; CURRENT FILING DATE: 2002-06-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phagotope
US-10-156-820-59

Query Match 53.1%; Score 17; DB 13; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLLT 4
:||||
Db 3 YTLT 6

RESULT 14
US-10-097-175-97
; Sequence 97, Application US/10097175
; Publication No. US20030045680A1
; GENERAL INFORMATION:
; APPLICANT: JOYAL, JOHN L.
; APPLICANT: MUELLER, JOHN
; APPLICANT: OZA, VISHA B.
; APPLICANT: FINDELS, MARK A.
; TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR
; FILE REFERENCE: PFI-110
; CURRENT APPLICATION NUMBER: US/10/097,175
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/275,240
; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: 60/352,399
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Androgen Receptor Binding Polypeptides
US-10-097-175-97

Query Match 53.1%; Score 17; DB 14; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTISS 7
:||||
Db 1 LTIES 5

RESULT 15
US-10-698-489-17
; Sequence 17, Application US/10698489
; Publication No. US20040067523A1
; GENERAL INFORMATION:
; APPLICANT: MERRILOV, Gennady et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103CON
; CURRENT APPLICATION NUMBER: US/10/698,489
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: To Be Assigned
; PRIOR FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: 09/777,921
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-489-17

Query Match 53.1%; Score 17; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 6
:||||
Db 2 LTIS 5

Search completed: November 4, 2004, 01:43:16
Job time : 70.6667 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2004, 01:09:31 ; Search time 18.3333 Seconds
(without alignments)
36.737 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	11	34.4	4	2 A40135	branched-chain-ami
2	11	34.4	5	2 B44817	34.5K structural p
3	11	34.4	5	2 D44817	35K structural pro
4	11	34.4	5	2 P06644	T-cell receptor be
5	10	31.2	7	2 E30608	Ig kappa chain V-I
6	9	28.1	3	3 T13892	cytochrome-c oxida
7	9	28.1	5	2 E60274	major protein anti
8	9	28.1	5	2 A37114	hypoxanthine phosph
9	9	28.1	5	2 H44817	34.5K structural p
10	9	28.1	5	2 P44817	34.5K structural p
11	9	28.1	5	2 S9237	surface protein te
12	9	28.1	5	2 D42364	flagellar protein te
13	9	28.1	6	2 A50985	N-formyl oligopept
14	9	28.1	6	2 S14159	paraspinal crystal
15	9	28.1	6	2 A43766	28K ubiquitin-immu
16	9	28.1	6	2 I37263	Y protein - human
17	9	28.1	6	2 I65546	MHC H2-L antigen -
18	9	28.1	7	2 S25266	p1E protein - Esc
19	9	28.1	7	2 P30254	18K protein 5507 -
20	9	28.1	7	2 P06649	pullulanase (EC 3.
21	9	28.1	7	2 S09066	Globulin IV alpha
22	9	28.1	7	2 A25269	sex pheromone cM3
23	9	28.1	7	2 A30812	sex pheromone cCF1
24	8	25.0	3	3 P70622	T-cell receptor be
25	8	25.0	4	2 P70696	T-cell receptor be
26	8	25.0	4	2 P70645	T-cell receptor be
27	8	25.0	4	2 P70712	T-cell receptor be
28	8	25.0	4	2 P70698	T-cell receptor be
29	8	25.0	4	2 P70551	T-cell receptor be

30	8	25.0	4	2 PT0697	T-cell receptor be
31	8	25.0	5	2 I39964	ribosomal protein
32	8	25.0	5	2 I39966	ribosomal protein
33	8	25.0	5	2 I39965	ribosomal protein
34	8	25.0	5	2 T10954	hypothetical prote
35	8	25.0	5	2 I50385	myosin light chain
36	8	25.0	5	2 PT0308	Ig heavy chain CRD
37	8	25.0	5	2 PT0596	T-cell receptor be
38	8	25.0	5	2 PT0610	T-cell receptor be
39	8	25.0	5	2 PT0597	T-cell receptor be
40	8	25.0	5	2 PT0729	T-cell receptor be
41	8	25.0	5	2 PT0624	T-cell receptor be
42	8	25.0	5	2 PT0625	T-cell receptor be
43	8	25.0	5	2 PT0672	T-cell receptor be
44	8	25.0	5	2 PT0660	T-cell receptor be
45	8	25.0	5	2 PT0656	T-cell receptor be

ALIGNMENTS

RESULT 1
A40135
branched-chain-amino-acid transferase (EC 2.6.1.42), mitochondrial - rat (fragment)
N:Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
C:Accession: A40135
R:Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A:Reference number: A40135
A:Accession: A40135
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <HUT>
C:Keywords: aminotransferase; mitochondrion

Query Match 34.4%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
Db 1 VSS 3

RESULT 2

B44817
34.5K structural protein - Leuconostoc oenos phase PZt11-15 (fragment)
C:Species: Leuconostoc oenos phase PZt11-15
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: B44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A>Title: Lysogeny in Leuconostoc oenos
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: B44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTSS 7
Db 1 LATSS 5

RESULT 3

D44817
35K structural protein - Leuconostoc oenos phase Pat5-12 (fragment)

C;Species: Leuconostoc oenos phage PAT5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
R;Arndt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos
A;Reference number: A44817; MUID:92085033; PMID:1748868
A;Accession: D44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTIS 7
DB 1 LATSS 5

RESULT 4

PT0644
T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0644
R;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0644
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Cross-references: UNIPROT:Q9Z2T6
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.4%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
DB 4 FT 5

RESULT 5

E30608
Ig kappa chain V-III region (Gag) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Accession: E30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: E30608
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <GON>
C;Keywords: heterotetramer; immunoglobulin

Query Match 31.2%; Score 10; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTIS 6
DB 4 LTQS 7

RESULT 6

TI3892
cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fra
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: TI3892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the CC
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Accession: TI3892
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3
A;Cross-references: EMBL:Y09528; NID:G2340016; PIDN:CAA70721.1; PID:G4379123
C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 28.1%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
DB 2 TL 3

RESULT 7

E60274
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wilker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the cultur
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTILT 4
DB 2 YPIT 5

RESULT 8

A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (frag
C;Species: Schistosoma mansoni
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C;Accession: A37114
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Fu
A;Reference number: A37114; MUID:90337955; PMID:2199439
A;Accession: A37114
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <YUA>
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
: ||
Db 1 MSS 3

RESULT 9

H44817

34.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C:Species: Leuconostoc oenos phase P32
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysozyme in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTISS 7
: ||
Db 1 MATSS 5

RESULT 10

F44817

34.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C:Species: Leuconostoc oenos phase P54
C>Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysozyme in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LTISS 7
: ||
Db 1 MATSS 5

RESULT 11

S69237

surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)
C:Species: Staphylothermus marinus
C>Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C:Accession: S69237
R:Persers, J.; Nitsch, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh
J. Mol. Biol. 245, 385-401, 1995
A:Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua
A:Reference number: S69237; MUID:95139068; PMID:7837271
A:Accession: S69237
A:Molecule type: protein
A:Residues: 1-5 <RET>
A:Experimental source: strain FI, DSM 3639
C:Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
: ||
Db 2 TL 3

RESULT 12

E42364

flagellar protein flir - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: E42364
R:Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A:Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and s
A:Reference number: A42364; MUID:91258342; PMID:1646201
A:Accession: E42364
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5 <VOG>
A:Cross-references: UNIPROT:P26416; GB:M62408

Query Match 28.1%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
: ||
Db 3 TL 4

RESULT 13

A60986

N-formyl oligopeptide - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
C:Accession: A60986
R:Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A:Title: Purification and amino acid sequencing of naturally occurring N-formyl-methion
A:Reference number: A60986; MUID:90092408; PMID:2689204
A:Accession: A60986
A:Molecule type: protein
A:Residues: 1-6 <BRO>

Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PTL 3
: ||
Db 3 FIL 5

RESULT 14

S14159

parasporal crystal protein CryIC - Bacillus thuringiensis (fragment)
N:Alternate names: delta-endotoxin
C:Species: Bacillus thuringiensis
C>Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: S14159
R:Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
A:Title: Two structural domains as a general fold of the toxic fragment of the Bacillus
A:Reference number: S14087; MUID:91153300; PMID:1847885
A:Accession: S14159
A:Molecule type: protein
A:Residues: 1-6 <CON>

Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ISS 7
||:
Db 1 IST 3

RESULT 15

A43766
28K ubiquitin-immunoreactive protein - inky cap (Coprinus cinereus) (fragment)
C:Species: Coprinus cinereus
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993
C:Accession: A43766
Rikanda, T.; Inoue, M.; Akiyama, M.
Biochimie 72, 355-359, 1990
A:Title: Purification and characterization of an ubiquitin-immuno-reactive protein local
A:Reference number: A43766; MUID:91002724; PMID:1698461
A:Accession: A43766
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-6 <KAN>

Query Match 28.1%; Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
||
Db 5 TL 6

Search completed: November 4, 2004, 01:24:17
Job time : 18.3333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:55:00 ; Search time 99.6667 seconds
(without alignments)
40.411 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	16	50.0	7	P70804	azotobacter
2	12	37.5	7	GFRP_MOUSE	mus musculus
3	12	37.5	7	O34028	spingomona
4	11	34.4	5	RE31_LITRU	litoria rub
5	11	34.4	5	RE32_LITRU	litoria rub
6	11	34.4	7	P83530	lactobacill
7	11	34.4	7	Q54248	streptomyce
8	10	31.2	5	E104_LITRU	litoria rub
9	10	28.1	6	P83533	lactobacill
10	9	28.1	7	CCF1_ENTFA	enterococcu
11	9	28.1	7	C1A_ENTFA	enterococcu
12	9	28.1	7	P82445	enterococcu
13	9	28.1	7	O07354	nicotiana t
14	9	28.1	7	Q8JE81	synechococc
15	8	25.0	5	ALL14_CARMA	human immun
16	8	25.0	5	B10B_CITFR	carcinus ma
17	8	25.0	5	PSK_DAUCA	citrobacter
18	8	25.0	5	LOK1_LOCMI	gaucus caro
19	8	25.0	6	P82181	locusta mig
20	8	25.0	6	P82182	spinacia ol
21	8	25.0	7	ALL2_CARMA	spinacia ol
22	8	25.0	7	ALL3_CARMA	carcinus ma
23	8	25.0	7	ALL4_CARMA	carcinus ma
24	8	25.0	7	ALL5_CARMA	carcinus ma
25	8	25.0	7	ALL7_CYPDO	cydia pomon
26	8	25.0	7	UC24_MAIZE	zea mays (m
27	8	25.0	7	Q8TAQ4	homo sapien
28	8	25.0	7	P72081	nocardia la
29	7	21.9	4	E0SI_HUMAN	homo sapien
30	7	21.9	4	YIM1_YEAST	saccharomyc
31	7	21.9	5	B10A_CITFR	citrobacter

32	7	21.9	6	1	UN06_CLOPA	P81351	clostridium
33	7	21.9	7	2	P83492	P83492	bionectria
34	7	21.9	7	2	Q47029	Q47029	enterobacte
35	7	21.9	7	2	Q65578	Q65578	bovine herp
36	6	18.8	4	1	ACH1_ACHFU	P35904	achatina fu
37	6	18.8	4	1	FAR3_HIRME	P42862	hirudo medi
38	6	18.8	4	1	FAR4_HIRME	P42862	hirudo medi
39	6	18.8	4	1	FFRA_ATEL	P58705	anthopleura
40	6	18.8	4	1	FLRF_HIRME	P42561	hirudo medi
41	6	18.8	4	1	FLRN_ATEL	P58707	anthopleura
42	6	18.8	4	1	FMRF_MACNI	P01162	macrocallis
43	6	18.8	4	1	FYRI_ATEL	P58706	anthopleura
44	6	18.8	4	1	OCPI_OCTMI	P58648	octopus min
45	6	18.8	4	2	Q16047	Q16047	homo sapien

ALIGNMENTS

RESULT 1

P70804 PRELIMINARY; PRT; 7 AA.
 ID P70804
 AC P70804;
 DT 01-FEB-1997 (Tremblrel. 02, Created)
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Algt protein (fragment).
 GN Name=algt;
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=E;
 RX MEDLINE=96427318; PubMed=8830682;
 RA Rehm B.H.A., Ertesvag H., Valla S.;
 RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
 part of an alg gene cluster physically organized in a manner similar
 to that in Pseudomonas aeruginosa.";
 RL J. Bacteriol. 178:5884-5889(1996).
 DR EMBL; X87973; CAA61230.1; -.
 FT NON TER 1
 SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;
 Query Match 50.0%; Score 16; DB 2; Length 7;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TISS 7

Db 2 TVSS 5

RESULT 2

GFRP_MOUSE STANDARD; PRT; 7 AA.
 ID GFRP_MOUSE
 AC P99025;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
 GN Name=Gchfr; Synonyms=Gfrp;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Prutiger S., Hughes G., Yan J.X.,
 Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
 Submitted (AUG-1998) to Swiss-Prot.

CC -1- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC SWISS-2DPAGE; P99025; MOUSE.
DR Direct protein sequencing.
KW INIT MET 0
FT NON TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 37.5%; Score 12; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LTISS 7
DB 3 LLISS 7

RESULT 3
RE31_LITRU PRELIMINARY; PRT; 7 AA.
ID O34028
AC O34028;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Catechol-2,3-dioxygenase (Fragment).
GN Name=pheN;
OS Sphingomonas chumuckensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=56193;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DJ77;
RA Kim Y.-C.; (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88298; AAB66311.1; -.
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
KW Dioxygenase.
FT NON TER 1
SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;

Query Match 37.5%; Score 12; DB 2; Length 7;
Best Local Similarity 20.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTISS 7
DB 3 MTVNT 7

RESULT 4
RE31_LITRU STANDARD; PRT; 5 AA.
ID P82072;
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidæ;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinbörner S.T.; Wabnitz P.A.; Waugh R.J.; Bowie J.H.; Gao C.;
RA Tyler M.J.; Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";

RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5
FT Threonine amide.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
DB 4 FT 5

RESULT 5
RE32_LITRU STANDARD; PRT; 5 AA.
ID P82073;
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidæ;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
'Litoria rubella'. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 34.4%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FT 2
DB 4 FT 5

RESULT 6
P83530 PRELIMINARY; PRT; 7 AA.
ID P83530;
AC P83530;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=1112860;
RA Drews O.; Weiss W.; Reil G.; Parlar H.; Wait R.; Goerg A.;

```

RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLT 5
Db 2 TLDV 5

RESULT 7
ID Q54248 PRELIMINARY; PRT; 7 AA.
AC Q54248;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Rp10 protein (Fragment).
GN Name=rp10;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2-3-11;
RX MEDLINE=20011291; PubMed=10542330;
RA Poehling S., Piepersberg W., Wehmeier U.F.;
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
RT N2-3-11 and interaction of the SecY protein with the SecA protein.";
RL Biochim. Biophys. Acta 1447:298-302(1999).
DR EMBL; X95915; CAA65160.1; -.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 34.4%; Score 11; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLT 4
Db 2 TLT 4

RESULT 8
ID E104_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 Histidine amide.
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 31.2%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LTI 5
Db 2 ITV 4

RESULT 9
ID P83533 PRELIMINARY; PRT; 6 AA.
AC P83533;
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 20451;
RX PubMed=12112860;
RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT "High pressure effects step-wise altered protein expression in
RT Lactobacillus sanfranciscensis.";
RL Proteomics 2:765-774(2002).
CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC protein is: 15 kDa.
FT NON_TER 1 1
FT NON_TER 6 6
FT NON_TER 5 5
SQ SEQUENCE 6 AA; 590 MW; 6DDDD452D1AAC000 CRC64;

Query Match 31.2%; Score 10; DB 2; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.8e+06;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TISS 7
Db 2 TVNA 5

RESULT 10
ID CCF1_ENTFA STANDARD; PRT; 7 AA.
AC C20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=8900813; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adsit J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative
RT transfer of the Streptococcus faecalis tetracycline resistance
RT plasmid, pCF10.";
RL J. Biol. Chem. 263:14574-14578(1988).
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the
CC hemolysin plasmid pCF10.
CC PIR; A30812; A30812.

```

Thu Nov 4 07:26:59 2004

us-09-712-819d-1.closed.rup

KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
|
|
Db 3 TL 4

RESULT 11
C1A_ENTFA STANDARD; PRT; 7 AA.
ID C1A_ENTFA
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (C1A).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RW SEQUENCE.
RP MEDLINE=87005252; PubMed=3093276;
RX Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373.";
RL FEBS Lett. 206:69-72 (1986).
CC -!- FUNCTION: CAM373 induces mating response of donor cells harboring
CC PAM373.
CC -!- MISCELLANEOUS: The N-terminus is possibly responsible for
CC specificity of pheromones to plasmids.
DR PIR; A25269; A25269.
KW Direct protein sequencing; Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 28.1%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.9e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
|
|
Db 3 FIL 5

RESULT 12
P82445 PRELIMINARY; PRT; 7 AA.
ID P82445
AC P82445;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 10 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RW SEQUENCE.
RP STRAIN=cv. PETIT HAVANA;
RX Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Woitaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0 (2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.

FT NON TER 7 758 MW; 69D2C1E862D1E2A0 CRC64;
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1E2A0 CRC64;

Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.8e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LTI 5
|
|
Db 1 VIV 3

RESULT 13
O07354 PRELIMINARY; PRT; 7 AA.
ID O07354
AC O07354;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NifK (Fragment).
GN Name-nifK;
OS Synchococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RW SEQUENCE FROM N.A.
RP STRAIN=RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synchococcus sp. strain
RF-1.";
RL Microbiology 145:743-753 (1999).
DR EMBL; AF003700; AAC35193.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;

Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
|
|
Db 3 FDL 5

RESULT 14
Q8JEB1 PRELIMINARY; PRT; 7 AA.
ID Q8JEB1
AC Q8JEB1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name-pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RW SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276 (2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 28.1%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TL 3
Db 4 TL 5

RESULT 15

ALI4_CARMA
ID ALI4_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Fortunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H.; Johnsen A.H.; Maestro J.-L.; Scott A.G.; Jaros P.P.;
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD RES 5 5 Leucine amide (Potential).
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 25.0%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTL 3
Db 3 FGL 5

Search completed: November 4, 2004, 01:23:16
Job time : 100.667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:54:10 ; Search time 92.3333 seconds
(without alignments)
27.196 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FILTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 116873

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	87.5	7	2	AAY40738 S4 deriva
2	28	87.5	7	3	AAB30076 Scaffold
3	25	78.1	7	2	AAY40737 S4 deriva
4	25	78.1	7	3	AAB30075 Scaffold
5	24	75.0	7	2	AAY40736 S4 deriva
6	24	75.0	7	3	AAB30074 Scaffold
7	22	68.8	6	8	ADG33308 Scaffold
8	21	65.6	7	2	AAY40735 S4 deriva
9	21	65.6	7	3	AAB30073 Scaffold
10	20	62.5	5	5	AAU85454 Human col
11	20	62.5	6	8	ADP29477 Human sec
12	19	59.4	6	4	AAU51422 Integrin
13	18	56.2	5	6	ABR55418 Amino aci
14	18	56.2	7	2	AAW58711 Tryptic 4
15	18	56.2	7	3	AAU64225 Cadherin-
16	18	56.2	7	5	ABG34102 Human sin
17	18	56.2	7	8	ADG33396 Tryptic 4
18	18	56.2	7	8	ADG33396 Tryptic 4
19	17	53.1	5	6	ABU12234 Streptoco
20	17	53.1	6	2	AAW12235 Hexapepti
21	17	53.1	6	2	AAW39453 Human T c
22	17	53.1	6	2	AAW75358 Hexapepti
23	17	53.1	6	2	AAW75290 Hexapepti
24	17	53.1	6	6	AAE31832 Androgen
25	17	53.1	6	8	ADL15755 Novel tra

ALIGNMENTS

RESULT 1

AAAY40738
ID AAY40738 standard; peptide; 7 AA.

XX AAY40738;

DT 01-DEC-1999 (first entry)

DE S4 derivative #12, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.

XX Synthetic.

PN EP947582-A1.

PD 06-OCT-1999.

PF 31-MAR-1998; 98EP-00870065.

PR 31-MAR-1998; 98EP-00870065.

XX (INNO-) INNOGENETICS NV.

PA Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

PT New scaffold protein, useful for stabilizing antigens used as vaccines.

PS Disclosure; Page 6; 105pp; English.

CC Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

Aar07656 Ribonucle
Aay40723 S3 deriva
Aab30062 Scaffold
Aam44200 H11 bindi
Aam44205 H11 bindi
Aap93345 Portion o
Aar93089 GAL4 DNA
Aaw61443 Gal 4 pro
Aaw76753 Murine si
Aaw92487 Murine Ga
Aay90491 GAL4 DNA
Aab03571 Nuclear c
Aab36961 Peptide #
Aab60836 Peptide #
Abj11455 Human 125
Aae28111 Human imm
Aab72693 Novel pro
Aar45358 Staphyloc
Aar46478 Staphyloc
Aar44966 Staphyloc

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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines

Sequence 7 AA;

Query Match 87.5%; Score 28; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
DB 2 FTLTIS 7

RESULT 2
AAB30076
ID AAB30076 standard; peptide; 7 AA.
AC AAB30076;
DT 09-FEB-2001 (first entry)
XX Scaffold protein SCA S4 peptide SEQ ID NO: 137.

Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.

Synthetic.
WO2000060070-A1.
12-OCT-2000.
01-APR-1999; 99WO-EP002283.
01-APR-1999; 99WO-EP002283.
(INNO-) INNOGENETICS NV.
Desmet J, Hufton S, Hoogenboom H, Sablon E;
WPI; 2000-665002/64.
Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
Disclosure; Page 15; 68pp; English.

The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention

Sequence 7 AA;

Query Match 87.5%; Score 28; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
DB 1 FTLTIS 7

Db 2 FTLTIS 7

RESULT 3
AAY40737
ID AAY40737 standard; peptide; 7 AA.
XX AAY40737;
AC AAY40737;
DT 01-DEC-1999 (first entry)
XX S4 derivative #11, beta strand of scaffold protein structure.

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
tumour; chemotherapeutic agent.
Synthetic.
EP947582-A1.
06-OCT-1999.
31-MAR-1998; 98EP-00870065.
31-MAR-1998; 98EP-00870065.
(INNO-) INNOGENETICS NV.

Desmet J, Hufton S, Hoogenboom H, Sablon E;
WPI; 1999-542958/46.
New scaffold protein, useful for stabilizing antigens used as vaccines.
Disclosure; Page 6; 105pp; English.

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines

Sequence 7 AA;

Query Match 78.1%; Score 25; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
DB 2 YTLTIS 7

RESULT 4

AAB30075
ID AAB30075 standard; peptide; 7 AA.
XX
AC AAB30075;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 136.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
XX WO200060070-A1.
XX
XX 12-OCT-2000.
XX
PF 01-APR-1999; 99WO-EP002283.
XX
PR 01-APR-1999; 99WO-EP002283.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
XX WPI; 2000-665002/64.
XX
DR Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
XX Disclosure; Page 15; 68pp; English.
XX
XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
SQ Sequence 7 AA;
Query Match 78.1%; Score 25; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTIS 6
Db :|||||
2 YTLTIS 7
RESULT 5
AAY40736
ID AAY40736 standard; peptide; 7 AA.
XX
AC AAY40736;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #10, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
XX EP947582-A1.
PN
PD 06-OCT-1999.
XX
XX

PF 31-MAR-1998; 98EP-00870065.
XX
PR 31-MAR-1998; 98EP-00870065.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX
XX WPI; 1999-542958/46.
DR
XX New scaffold protein, useful for stabilizing antigens used as vaccines.
PT
XX Disclosure; Page 6; 105pp; English.
XX
XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
CC S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
CC beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
CC Y40609) together form a single-chain scaffold protein which contains at
CC least 1 disulfide bond, contains less than 10% alpha helix and contains
CC at least 6 beta-strands. The scaffold protein is constructed of beta
CC strands S1-S6, and may also include beta strands A1-A3, or any
CC functionally equivalent derivative of these sequences. The beta strands
CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;
Query Match 75.0%; Score 24; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTIS 6
Db :|||||
2 FTLSIS 7
RESULT 6
AAB30074
ID AAB30074 standard; peptide; 7 AA.
XX
AC AAB30074;
XX
DT 09-FEB-2001 (first entry)
XX
DE Scaffold protein SCA S4 peptide SEQ ID NO: 135.
XX
KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.
XX
OS Synthetic.
XX
XX WO200060070-A1.
PN
XX 12-OCT-2000.
PD
XX 01-APR-1999; 99WO-EP002283.
PF
XX 01-APR-1999; 99WO-EP002283.
PR

Thu Nov 4 07:26:57 2004

CC hard acid cation chelator at X or Y, and a soft acid cation chelator at
CC remaining X or Y. The hard acid cation chelator includes a carboxylate or
CC amine group. It comprises NOTA (1,4,7-triazacyclononane-N,N',N''-triacetic
CC acid), DOTA (1,4,7,10-tetraazacyclododecanetetraacetic acid), DTPA
CC (diethylenetriaminepentaacetic acid), or TETA (p-bromoacetamido-benzyl-
CC tetraethylenetetraacetic acid). It includes a cation consisting of
CC Group IIA or Group IIB metal cations. The soft acid cation chelator
CC includes a thiol group. It comprises Tscg-Cys
CC (thiosemicarbazonylglycylcysteine) or Tscg-Cys
CC (thiosemicarbazonylacetylcysteine). It includes a cation consisting of
CC transition metals, lanthanides, actinides, Tc, Re or Bi. The compound is
CC useful for preparing a composition for diagnosing or treating tumor or
CC infections caused by fungus, virus, parasite, bacterium, protozoan or
CC mycoplasma. The invention also discloses that the peptide of the
CC invention can be fused or recognised and bound by an antibody, especially
CC a bispecific single chain antibody. This sequence corresponds to the last
CC 6 amino acids of the heavy chain variable region from the human 734
CC antibody. The peptide sequence is used to generate a fusion antibody or
CC fragment that will recognise and bind the peptides of the invention.
XX
SQ Sequence 6 AA;

Query Match 68.8%; Score 22; DB 8; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTSS 7
Db 1 TTVSS 6

RESULT 8
AAY40735
ID AAY40735 standard; peptide; 7 AA.
XX
AC AAY40735;
XX
DT 01-DEC-1999 (first entry)
XX
DE S4 derivative #9, beta strand of scaffold protein structure.
XX
KW Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
KW tumour; chemotherapeutic agent.
XX
OS Synthetic.
XX
XX EP947582-A1.
XX
PD 06-OCT-1999.
XX
XX 31-MAR-1998; 98EP-00870065.
XX
XX 31-MAR-1998; 98EP-00870065.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 1999-542958/46.
XX
XX New scaffold protein, useful for stabilizing antigens used as vaccines.
XX
XX Disclosure; Page 6; 105pp; English.
XX
XX Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
XX S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a
XX beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-
XX Y40609) together form a single-chain scaffold protein which contains at
XX least 1 disulfide bond, contains less than 10% alpha helix and contains
XX at least 6 beta-strands. The scaffold protein is constructed of beta
XX strands S1-S6, and may also include beta strands A1-A3, or any
XX functionally equivalent derivative of these sequences. The beta strands
XX form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to

XX
PA (INNO-) INNOGENETICS NV.
XX
PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
XX WPI; 2000-665002/64.
XX
XX Scaffold composed of single-chain polypeptide having beta sandwich
XX architecture carrying new and randomized peptide sequences useful as
XX supporting framework and carrying antigen- or receptor binding fragments.
XX
XX Disclosure; Page 15; 68pp; English.
XX
XX The present invention is concerned with producing scaffold proteins based
XX upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
XX a scaffold to bind antigen- or receptor-binding fragments. These can be
XX used in the treatment of diseases such as cancer, atherosclerosis,
XX thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
XX Sequences AAB29930-B29939 were used in the production of the proteins of
XX the invention
XX
SQ Sequence 7 AA;

Query Match 75.0%; Score 24; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db 2 FTLTIS 7

RESULT 7
ADG63308
ID ADG63308 standard; peptide; 6 AA.
XX
AC ADG63308;
XX
XX 11-MAR-2004 (first entry)
XX
DE Antibody 734 heavy chain variable region last 6 amino acids.
XX
XX cytostatic; virucide; antifungal; antiparasitic; antibacterial;
KW protozoicide; gene therapy; diagnosis; tumor; fungus; virus; parasite;
KW bacterium; protozoan; mycoplasma; acid cation chelator.
XX
XX Homo sapiens.
XX
XX WO2003097105-A1.
XX
XX 27-NOV-2003.
XX
XX 16-MAY-2003; 2003WO-GB002110.
XX
XX 17-MAY-2002; 2002US-00150654.
XX
XX (IMMU-) IMMUNOMEDICS INC.
XX
XX (MCCA/) MCCALL J D.
XX
XX Goldenberg DM, Hansen H, Leung S, McBride WJ, Qu Z;
XX WPI; 2004-042533/04.
XX
XX New compound, useful for preparing a composition for diagnosing or
XX treating tumor or infections caused by fungus, virus, parasite,
XX bacterium, protozoan or mycoplasma.
XX
XX Example 24; SEQ ID NO 18; 119pp; English.
XX
XX The invention relates to a compound, useful for preparing a composition
XX for diagnosing or treating tumor or infections caused by fungus, virus,
XX parasite, bacterium, protozoan or mycoplasma, comprising the formula (I):
XX X-Phe-Lys (HSG)-D-Tyr-Lys (HSG)-Lys (Y)-NH₂ (I). The compound includes a

CC the next by hydrogen bonds, which generate a beta sandwich architecture.
CC If the additional beta strands A1-A3 are included in the structure the
CC scaffold is constructed of two beta sheets, with the structures
CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
CC other via amino acid loops, where at least one of the loops binds to a
CC receptor or antigen. The scaffold protein is used to stabilize antigens
CC or whole proteins such as receptors, or their fragments. It may be used
CC to bind two separate molecules. For example, one surface of the scaffold
CC may be bound to a protein which binds to a tumour antigen. This will
CC target the complex to tumour cells. Another surface may be bound to a
CC cytotoxic molecule or an autoimmune antibody which may then kill the
CC tumour cells. Therefore the scaffold protein may be used to target
CC chemotherapeutic agents to specific cells. It may also be used to
CC stabilize individual peptides in a peptide library and may be used in
CC diagnostic techniques, and to stabilize antigens used as vaccines
XX
SQ Sequence 7 AA;

Query Match 65.6%; Score 21; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db 2 YSLTIS 7
::|||

RESULT 9
AAB30073
ID AAB30073 standard; peptide; 7 AA.

AC AAB30073;

DT 09-FEB-2001 (first entry)

DE Scaffold protein SCA S4 peptide SEQ ID NO: 134.

XX Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
KW diabetic retinopathy; atherosclerosis.

OS Synthetic.

XX W0200060070-A1.

XX 12-OCT-2000.

XX 01-APR-1999; 99WO-EP002283.

XX 01-APR-1999; 99WO-EP002283.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 2000-665002/64.

XX Scaffold composed of single-chain polypeptide having beta sandwich
PT architecture carrying new and randomized peptide sequences useful as
PT supporting framework and carrying antigen- or receptor binding fragments.
XX
XX Disclosure; Page 15; 68pp; English.

XX The present invention is concerned with producing scaffold proteins based
CC upon the human CTLA-4 SCA domain. These scaffold proteins can be used as
CC a scaffold to bind antigen- or receptor-binding fragments. These can be
CC used in the treatment of diseases such as cancer, atherosclerosis,
CC thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy.
CC Sequences AAB29930-B29939 were used in the production of the proteins of
CC the invention
XX
XX Sequence 7 AA;

Query Match 65.6%; Score 21; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTIS 6
Db 2 YSLTIS 7
::|||

RESULT 10
AAU85454
ID AAU85454 standard; peptide; 5 AA.

XX AC AAU85454;

XX DT 21-MAY-2002 (first entry)

XX Human colon specific polypeptide antibody binding site #31.
DE Human; colon specific gene; CSG; cytostatic; metastasis;
KW colon cancer staging; antibody binding site.

XX OS Homo sapiens.

XX PN W0200206515-A2.

XX PD 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US022454.

XX 17-JUL-2000; 2000US-00618596.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Sun Y;

XX WPI; 2002-171815/22.

XX Diagnosing, staging or monitoring colon cancer involves determining a
PT colon specific gene in cells, tissues or body fluids in patient, and
PT comparing it with levels of the gene from a normal human control.
XX
XX Disclosure; Page 21; 52pp; English.

XX The invention relates to diagnosing the presence of colon cancer,
CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
CC for the onset of metastasis or monitoring a change in stage of colon
CC cancer in a patient. The method involves determining a colon specific
CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
CC levels of CSG in cells, tissues or bodily fluids from a normal human
CC control. Colon cancer can be treated by administering a molecule which
CC down regulates the expression or activity of CSG. An immune response
CC against a target cell expressing CSG can be induced by delivering an
CC immunologically stimulatory amount of a CSG protein to a patient, so that
CC an immune response is mounted. Therapeutic agents are useful for imaging
CC colon cancer in a patient by administering an agent labelled with
CC paramagnetic ions or a radioisotope to the patient. They are also useful
CC for preventing the onset of colon cancer, and in diagnosis and treatment
CC of the disease. Sequences AAU85424-AAU85502 represent human colon
CC specific protein antibody binding sites used in the method of the
CC invention
XX
XX Sequence 5 AA;

Query Match 62.5%; Score 20; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLT 4
Db 2 FTLT 5
|||

RESULT_11

ID	ADP29477	standard; protein; 6 AA.
AC	ADP29477;	
DT	12-AUG-2004	(first entry)
XX	Human secreted protein SEQ ID #244.	
DE	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; inflammatory; immune; human secreted protein.	
OS	Homo sapiens.	
PX	WO2004035732-A2.	
PD	29-APR-2004.	
PF	28-AUG-2003;	2003WO-US026780.
PR	29-AUG-2002;	2002US-0406576P.
PR	29-AUG-2002;	2002US-0406579P.
PR	29-AUG-2002;	2002US-0406585P.
PR	29-AUG-2002;	2002US-0406588P.
PR	29-AUG-2002;	2002US-0406608P.
PR	29-AUG-2002;	2002US-0406611P.
PR	29-AUG-2002;	2002US-0406612P.
PR	29-AUG-2002;	2002US-0406616P.
PR	29-AUG-2002;	2002US-0406640P.
PR	29-AUG-2002;	2002US-0406642P.
PR	29-AUG-2002;	2002US-0406646P.
PR	29-AUG-2002;	2002US-0406653P.
PR	29-AUG-2002;	2002US-0406655P.
PR	29-AUG-2002;	2002US-0406666P.
PR	17-SEP-2002;	2002US-0410946P.
PR	17-SEP-2002;	2002US-0410947P.
PR	17-SEP-2002;	2002US-0410948P.
PR	17-SEP-2002;	2002US-0410949P.
PR	17-SEP-2002;	2002US-0410953P.
PR	17-SEP-2002;	2002US-0410957P.
PR	17-SEP-2002;	2002US-0410958P.
PR	17-SEP-2002;	2002US-0410959P.
PR	17-SEP-2002;	2002US-0410960P.
PR	17-SEP-2002;	2002US-0410961P.
PR	17-SEP-2002;	2002US-0410962P.
PR	17-SEP-2002;	2002US-0411019P.
PR	17-SEP-2002;	2002US-0411022P.
PR	17-SEP-2002;	2002US-0411023P.
PR	17-SEP-2002;	2002US-0411024P.
PR	17-SEP-2002;	2002US-0411032P.
PR	17-SEP-2002;	2002US-0411035P.
PR	17-SEP-2002;	2002US-0411037P.
PR	17-SEP-2002;	2002US-0411041P.
PR	17-SEP-2002;	2002US-0411045P.
PR	17-SEP-2002;	2002US-0411046P.
PR	17-SEP-2002;	2002US-0411048P.
PR	17-SEP-2002;	2002US-0411052P.
PR	17-SEP-2002;	2002US-0411055P.
PR	17-SEP-2002;	2002US-0411073P.
PR	17-SEP-2002;	2002US-0411082P.
PR	17-SEP-2002;	2002US-0411101P.
PR	17-SEP-2002;	2002US-0411111P.
PR	18-APR-2003;	2003US-0463700P.
PR	18-APR-2003;	2003US-0463708P.
PR	18-APR-2003;	2003US-0463716P.
PR	18-APR-2003;	2003US-0463732P.
PR	02-MAY-2003;	2003US-0467199P.
PR	02-MAY-2003;	2003US-0467201P.
PR	02-MAY-2003;	2003US-0467203P.
PR	02-MAY-2003;	2003US-0467230P.
PR	19-MAY-2003;	2003US-0471306P.
PR	19-MAY-2003;	2003US-0471336P.


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PR 22-MAY-2003; 2003US-0472420P.
PR 22-MAY-2003; 2003US-0472430P.
PR 09-JUN-2003; 2003US-0476609P.
PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485225P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX WPI; 2004-348438/32.
XX New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
PS Claim 1; SEQ ID NO 1475; 428pp; English.
XX The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, anti-inflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
XX Sequence 6 AA;
SQ Query Match 62.5%; Score 20; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 FTLT 4
DB 1 FTLT 4
|||||
RESULTS 12
AAAM51422
ID AAAM51422 standard; peptide; 6 AA.
AC AAAM51422;
XX AC AAAM51422;
DT DT 08-JAN-2002 (first entry)
XX XX Integrin activating peptide SEQ ID NO 1.
DE DE Integrin stimulant; vulnerary; injury healing; postsurgical tissue recovery.
KW KW Unidentified.
XX OS Unidentified.
XX JP2001213898-A.
XX PD 07-AUG-2001.
XX PF 31-JAN-2000; 2000JP-00022469.
XX PF 31-JAN-2000; 2000JP-00022469.
    
```


XX (HISM) HISAMITSU PHARM CO LTD.
 XX WPI; 2001-629610/73.
 XX An injury healing and postsurgical tissue recovering integrin activating
 PT peptide.
 XX
 PS Claim 1; Page 3; 11pp; Japanese.
 XX
 CC The invention relates to novel peptides with vulnerary activity, useful
 CC for injury healing and postsurgical tissue recovery by acting as an
 CC integrin stimulant
 XX
 SQ Sequence 6 AA;
 Query Match 59.4%; Score 19; DB 4; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.7e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTI 5
 Db 1 YTTTI 5
 :|||
 :|||

RESULT 13
 ABR55418
 ID ABR55418 standard; peptide; 5 AA.
 AC ABR55418;
 DT 29-JUL-2003 (first entry)
 XX
 DE Amino acid sequence of a conserved region of PLC-zeta protein.
 XX
 KW Phospholipase C zeta; PLC-zeta; calcium oscillation; oocyte; sperm;
 KW embryo; infertility.
 XX
 OS Unidentified.
 XX
 PN WC2003035678-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 18-OCT-2002; 2002WO-GB004739.
 XX
 PR 24-OCT-2001; 2001GB-00025498.
 PR 28-JUN-2002; 2002GB-00014945.
 XX
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
 XX
 PI Lai T;
 FI WPI; 2003-421400/39.
 DR
 XX New phospholipase C-zeta gene, useful for preparing a composition for
 PT diagnosing or treating infertility.
 XX
 PS Claim 10; Page 68; 107pp; English.
 XX
 CC ABR55412-20 represent conserved region of a phospholipase C (PLC)-zeta
 CC polypeptide. PLC-zeta polypeptides are capable of triggering calcium
 CC oscillations in oocytes. The PLC-zeta isoform is expressed specifically
 CC in mammalian sperm, and is an essential protein for mammalian
 CC fertilisation and embryo development. PLC-zeta polynucleotides are useful
 CC for preparing a composition for diagnosing or treating infertility
 XX
 SQ Sequence 5 AA;
 Query Match 56.2%; Score 18; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX (HISM) HISAMITSU PHARM CO LTD.
 XX WPI; 2001-629610/73.
 XX An injury healing and postsurgical tissue recovering integrin activating
 PT peptide.
 XX
 PS Claim 1; Page 3; 11pp; Japanese.
 XX
 CC The invention relates to novel peptides with vulnerary activity, useful
 CC for injury healing and postsurgical tissue recovery by acting as an
 CC integrin stimulant
 XX
 SQ Sequence 6 AA;
 Query Match 59.4%; Score 19; DB 4; Length 6;
 Best Local Similarity 60.0%; Pred. No. 1.7e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTI 5
 Db 1 YTTTI 5
 :|||
 :|||

RESULT 14
 AAW58711
 ID AAW58711 standard; peptide; 7 AA.
 AC AAW58711;
 DT 17-SEP-1998 (first entry)
 XX
 DE Tryptic 40 kD subunit CLMP peptide off PVDF #4.
 XX
 KW Cytotoxic lymphocyte maturation factor; CLMP; cytokine; synergize;
 KW interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying;
 XX proliferation; cytotoxic T cell; transplantation; antibody.
 OS Homo sapiens.
 XX
 PN US5780597-A.
 XX
 PD 14-JUL-1998.
 XX
 PF 02-JUN-1995; 95US-00460061.
 XX
 PR 22-DEC-1989; 89US-00455708.
 PR 09-MAY-1990; 90US-00520935.
 PR 27-AUG-1990; 90US-00572284.
 PR 24-MAR-1992; 92US-00857023.
 PR 02-MAR-1994; 94US-00205011.
 XX
 PA (HOFF) HOFFMANN LA ROCHE INC.
 XX
 PI Podlaski FJ, Stern AS, Gately MK, Pan YE, Hulmes JD;
 PI Chizzonite RA, Gubler UA;
 XX
 WPI; 1998-413150/35.
 XX
 XX New antibodies to cytotoxic lymphocyte maturation factor - useful for
 PT detecting, purifying, and/or blocking proliferation and activation of
 PT cytotoxic T cells, such as in transplantation(s).
 XX
 PS Example 3; Col 23; 71pp; English.
 XX
 CC An isolated antibody has been developed which binds specifically to
 CC cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF
 CC induced proliferation by more than 50% in a CLMF dependent T cell growth
 CC assay and/or inhibits binding of at least 60% of the factor to
 CC phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL)
 CC blasts as determined in a CLMF receptor binding assay. CLMF is a
 CC heterodimeric protein having a molecular weight band of 75 kD, determined
 CC by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC under non-reducing and/or reducing conditions, providing a first subunit
 CC having a molecular weight band of 40 kD and a second subunit having a
 CC molecular weight of 35 kD. The present sequence represents a tryptic 40
 CC kD CLMF peptide off polyvinylidene difluoride (PVDF), from an example of
 CC the present invention. The antibody can be used for the purification
 CC and/or detection of CLMF. It is also used in therapeutic treatments which
 CC require selective blocking of proliferation and activation of cytotoxic T
 CC cells (CTLs) such as in transplantation
 XX
 SQ Sequence 7 AA;
 Query Match 56.2%; Score 18; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TLTII 5
 Db 1 TLTII 4
 :|||
 :|||

Best Local Similarity 57.1%; Pred. No. 1.7e+06; Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
||: ||
Db 1 FTIDSS 7

Search completed: November 4, 2004, 01:18:12
Job time : 95.3333 secs

RESULT 15
AAV64225
ID AAY64225 standard; peptide; 7 AA.
XX AC
XX AAY64225;
XX
DT 02-MAR-2000 (first entry)
XX
DE Cadherin-related neuronal receptor CAR sequence SEQ ID NO:637.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease.
XX
OS Synthetic.
OS Homo sapiens.
XX
PW WO9957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA000363.
XX
PR 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00187859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX
XX WPI; 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
PS Claim 99; Page 216; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioeffectors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
SQ Sequence 7 AA;

Query Match 56.2%; Score 18; DB 3; Length 7;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 4, 2004, 00:42:19 ; Search time 16.6667 Seconds
(without alignments)
27.854 Million cell updates/sec

Title: US-09-712-819D-1
Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	25	5	PCT-US91-02942-26
2	32	100.0	25	5	PCT-US91-02942-42
3	32	100.0	32	2	US-08-470-139-13
4	32	100.0	32	3	US-08-569-147-40
5	32	100.0	32	3	US-09-347-061-13
6	32	100.0	32	3	US-09-425-638A-92
7	32	100.0	32	3	US-09-425-638A-94
8	32	100.0	32	3	US-09-543-004-92
9	32	100.0	32	3	US-09-543-004-94
10	32	100.0	32	4	US-09-647-468-129
11	32	100.0	32	4	US-09-563-222C-76
12	32	100.0	32	4	US-09-563-222C-86
13	32	100.0	32	4	US-09-563-222C-110
14	32	100.0	32	4	US-09-855-271-13
15	32	100.0	50	5	PCT-US91-02942-8
16	32	100.0	50	5	PCT-US91-02942-9
17	32	100.0	64	2	US-08-765-179B-10
18	32	100.0	64	2	US-08-765-179B-14
19	32	100.0	70	3	US-08-554-840-9
20	32	100.0	70	4	US-08-925-339-9
21	32	100.0	70	4	US-09-332-595-9
22	32	100.0	76	3	US-08-851-362D-21
23	32	100.0	80	3	US-08-554-840-10
24	32	100.0	80	3	US-08-554-840-12
25	32	100.0	80	3	US-08-554-840-13
26	32	100.0	80	3	US-08-554-840-15
27	32	100.0	80	4	US-08-925-339-10

28	32	100.0	80	4	US-08-925-339-12	Sequence 12, Appl
29	32	100.0	80	4	US-08-925-339-13	Sequence 13, Appl
30	32	100.0	80	4	US-08-925-339-15	Sequence 15, Appl
31	32	100.0	80	4	US-09-332-595-10	Sequence 10, Appl
32	32	100.0	80	4	US-09-332-595-12	Sequence 12, Appl
33	32	100.0	80	4	US-09-332-595-13	Sequence 13, Appl
34	32	100.0	80	4	US-09-332-595-15	Sequence 15, Appl
35	32	100.0	80	4	US-09-269-921-130	Sequence 130, App
36	32	100.0	93	3	US-08-783-853A-35	Sequence 35, Appl
37	32	100.0	93	3	US-09-344-050-35	Sequence 35, Appl
38	32	100.0	95	2	US-08-290-592E-19	Sequence 19, Appl
39	32	100.0	95	2	US-08-290-592E-33	Sequence 33, Appl
40	32	100.0	95	4	US-09-472-087-94	Sequence 94, Appl
41	32	100.0	95	5	PCT-US95-10053-16	Sequence 16, Appl
42	32	100.0	95	5	PCT-US95-10053-30	Sequence 30, Appl
43	32	100.0	95	5	PCT-US96-09448-19	Sequence 19, Appl
44	32	100.0	95	5	PCT-US96-09448-33	Sequence 33, Appl
45	32	100.0	96	3	US-08-466-368-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
PCT-US91-02942-26
; Sequence 26, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02942-26

Query Match 100.0%; Score 32; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 8 FTLTSS 14

RESULT 2

PCT-US91-02942-42
; Sequence 42, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02942-42

Query Match 100.0%; Score 32; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 8 FTLTSS 14

RESULT 3

US-08-470-139-13
; Sequence 13, Application US/08470139
; Patent No. 5998586
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,139
; FILING DATE: 06 JUNE-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: TRUJILLO, DOREEN YATKO

; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0044
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-139-13

Query Match 100.0%; Score 32; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 4

US-08-569-147-40
; Sequence 40, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-569-147-40

Query Match 100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 15 FTLTSS 21

RESULT 5

US-09-347-061-13
; Sequence 13, Application US/09347061

```
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Consensus
US-09-347-061-13

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
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Db 15 FTLTISS 21

RESULT 6
US-09-425-638A-92
; Sequence 92, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Weit and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-92

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 7
US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Weit and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; FEATURE:
US-09-425-638A-94

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 8
US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Weit and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-92

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 9
US-09-543-004-94
; Sequence 94, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Weit and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match          100.0%; Score 32; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
   |||||
Db 15 FTLTISS 21

RESULT 10
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US-09-647-468-129
; Sequence 129, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHICO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of FR3 of versions "a" of humanized L chain V
; OTHER INFORMATION: region
US-09-647-468-129

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
|||
Db 15 FTLTSS 21

RESULT 11
US-09-563-222C-76
; Sequence 76, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-76

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
|||
Db 15 FTLTSS 21

RESULT 12
US-09-563-222C-86
; Sequence 86, Application US/09563222C

; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-86

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
|||
Db 15 FTLTSS 21

RESULT 13
US-09-563-222C-110
; Sequence 110, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-110

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
|||
Db 15 FTLTSS 21

RESULT 14
US-09-855-271-13
; Sequence 13, Application US/09855271
; Patent No. 6734286
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088

; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-09-855-271-13

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 15
PCT-US91-02942-8
; Sequence 8, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ATHWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-8

Query Match 100.0%; Score 32; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
Db 26 FTLTISS 32

Search completed: November 4, 2004, 00:54:51
Job time : 17.6667 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:36:19 ; Search time 19 Seconds
(without alignments)
35.448 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32
Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	100.0	54	2 JT0521	Ig kappa chain V-I
2	32	100.0	71	2 S21526	Ig kappa chain V-I
3	32	100.0	77	2 S70443	Ig kappa chain V-I
4	32	100.0	77	2 D30502	Ig kappa chain V-I
5	32	100.0	78	2 S34102	Ig kappa chain V-I
6	32	100.0	79	2 S24215	Ig kappa chain V-I
7	32	100.0	81	2 PH1048	Ig kappa chain V-I
8	32	100.0	83	2 S78489	Ig kappa chain V-I
9	32	100.0	84	2 S34099	Ig kappa chain V-I
10	32	100.0	86	2 S16834	Ig kappa chain V-I
11	32	100.0	86	2 S16824	Ig kappa chain V-I
12	32	100.0	86	2 S16836	Ig kappa chain V-I
13	32	100.0	86	2 S16837	Ig kappa chain V-I
14	32	100.0	86	2 S16830	Ig kappa chain V-I
15	32	100.0	86	2 S16833	Ig kappa chain V-I
16	32	100.0	86	2 S16829	Ig kappa chain V-I
17	32	100.0	86	2 S16826	Ig kappa chain V-I
18	32	100.0	86	2 S34086	Ig kappa chain V-I
19	32	100.0	86	2 S16840	Ig kappa chain V-I
20	32	100.0	87	2 S34084	Ig kappa chain V-I
21	32	100.0	87	2 S21523	Ig kappa chain V-I
22	32	100.0	87	2 S34097	Ig kappa chain V-I
23	32	100.0	87	2 S34083	Ig kappa chain V-I
24	32	100.0	87	2 S34098	Ig kappa chain V-I
25	32	100.0	88	2 S21525	Ig kappa chain V-I
26	32	100.0	88	2 S21522	Ig kappa chain V-I
27	32	100.0	88	2 S21528	Ig kappa chain V-I
28	32	100.0	88	2 S21520	Ig kappa chain V-I
29	32	100.0	88	2 S34104	Ig kappa chain V-I

30	32	100.0	91	2 S37521	Ig kappa chain V-I
31	32	100.0	91	2 S37511	Ig kappa chain V-I
32	32	100.0	91	2 S37525	Ig kappa chain V-I
33	32	100.0	91	2 S37515	Ig kappa chain V-I
34	32	100.0	91	2 S37527	Ig kappa chain V-I
35	32	100.0	91	2 PH1071	Ig kappa chain V-I
36	32	100.0	92	2 S37504	Ig kappa chain V-I
37	32	100.0	92	2 S37509	Ig kappa chain V-I
38	32	100.0	92	2 S37506	Ig kappa chain V-I
39	32	100.0	92	2 S37512	Ig kappa chain V-I
40	32	100.0	92	2 S37522	Ig kappa chain V-I
41	32	100.0	92	2 S37532	Ig kappa chain V-I
42	32	100.0	92	2 S37533	Ig kappa chain V-I
43	32	100.0	92	2 S37530	Ig kappa chain V-I
44	32	100.0	92	2 S37523	Ig kappa chain V-I
45	32	100.0	92	2 S37535	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

JT0521
Ig kappa chain V-III region (CP1) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
C:Accession: JT0521
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A>Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157; PMID:2786547
A:Accession: JT0521
A:Molecule type: mRNA
A:Residues: 1-54 <ANK>
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-49/Domain: V region <VRE>
F:50-54/Domain: J region <JRE>

Query Match 100.0%; Score 32; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 23 FTLTSS 29

RESULT 2

S21526
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C:Accession: S34082; S21526
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A>Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed in a clonal fashion
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34082
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <WAZ>
A:Cross-references: EMBL:X66042; NID:G33318; PIDN:CAA46841.1; PID:G33319
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
Db 11 FTLTSS 29

Thu Nov 4 07:27:01 2004

us-09-712-819d-1.open.rpr

Db 64 FTLTISS 70

RESULT 3

S70443
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 07-May-1999
C:Accession: S70443
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fe
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70443
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-77 <GUI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 100.0%; Score 32; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 40 FTLTISS 46

RESULT 4

D30502
Ig kappa chain V region (D44) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Nov-1988 #sequence_revision 03-Aug-1992 #text_change 23-Jul-1999
C:Accession: D30502
R:Elia, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A:Reference number: A30502; MUID:88315787; PMID:2457627
A:Accession: D30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-77 <EIL>
A:Cross-references: GB:M21908; NID:G197073; PIDN:AAA38908.1; PID:G197074
A:Note: the authors translated the codon CAG for residue 48 as Pro
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 40 FTLTISS 46

RESULT 5

S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <WAG>
A:Cross-references: EMBL:X67186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 32; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 62 FTLTISS 68

RESULT 6

S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular exci
A:Reference number: S24214; MUID:91217618; PMID:1902500
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHI>
A:Cross-references: EMBL:X58202; NID:G53718; PIDN:CAA41178.1; PID:G930195
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 44 FTLTISS 50

RESULT 7

PH1048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1048
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0371; MUID:92381444; PMID:1512540
A:Accession: PH1048
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 32; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 56 FTLTISS 62

RESULT 8

S78489
Ig kappa chain V region (patient 28) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C:Accession: S78489; S34100
R:Wagner, S.
submitted to the EMBL Data Library, July 1992
A:Reference number: S78488

```
A:Accession: S78489
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: EMBL:X67184
A:Experimental source: patient 28
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34100
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown
A:Residues: 1-68, 'Q', 70-73, 'A', 75-83 <WAG>
A:Cross-references: EMBL:X67184
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:6-80/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
DB      61 FTLTISS 67

RESULT 9
S34099
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S34099
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34099
A:Molecule type: DNA
A:Residues: 1-84 <WAG>
A:Cross-references: UNIPROT:Q9UL83; EMBL:X67183
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:5-79/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
DB      60 FTLTISS 66

RESULT 10
S16834
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16834
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16834
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54832
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
DB      62 FTLTISS 68

RESULT 11
S16824
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16824
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fa
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16824
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54822
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
DB      62 FTLTISS 68

RESULT 12
S16836
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16836
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737; PMID:1903706
A:Accession: S16836
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54834
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match      100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
DB      62 FTLTISS 68

RESULT 13
S16837
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16837
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
```

Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; PMID:91243737; PMID:1903706
A:Accession: S16837
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54835
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTLTISS 7
Db 62 FTLTISS 68
Search completed: November 4, 2004, 00:48:40
Job time : 20 secs

Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; PMID:91243737; PMID:1903706
A:Accession: S16837
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54835
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTLTISS 7
Db 62 FTLTISS 68

RESULT 14
S16830
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16830
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; PMID:91243737; PMID:1903706
A:Accession: S16830
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54828
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>
Query Match 100.0%; Score 32; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTLTISS 7
Db 62 FTLTISS 68

RESULT 15
S16833
IG kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; PMID:91243737; PMID:1903706
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54831
A:Experimental source: clone bkv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLW>
A:Cross-references: EMBL:X54836
A:Experimental source: clone slkv14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

RESULT 15
S16833
IG kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; PMID:91243737; PMID:1903706
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54831
A:Experimental source: clone bkv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLW>
A:Cross-references: EMBL:X54836
A:Experimental source: clone slkv14
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:41:09 ; Search time 103 Seconds
(without alignments)
39.103 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	100.0	78	Q7VR58	Q7VR58 candidatus
2	32	100.0	81	AAR10995	Aar10995 mus muscu
3	32	100.0	93	AAR11030	Aar11030 mus muscu
4	32	100.0	101	AAR11008	Aar11008 mus muscu
5	32	100.0	107	KV1D_HUMAN	P01596 homo sapien
6	32	100.0	107	Q96SA9	Q96SA9 mus muscu
7	32	100.0	107	Q9ER29	Q9ER29 mus muscu
8	32	100.0	108	KV1F_HUMAN	P01598 homo sapien
9	32	100.0	108	KV1G_HUMAN	P01599 homo sapien
10	32	100.0	108	KV1H_HUMAN	P01600 homo sapien
11	32	100.0	108	KV1I_HUMAN	P01611 homo sapien
12	32	100.0	108	KV1S_MOUSE	P01650 mus muscu
13	32	100.0	108	KV5R_MOUSE	P01651 mus muscu
14	32	100.0	108	KV5S_MOUSE	P01652 mus muscu
15	32	100.0	108	KV5T_MOUSE	P01653 mus muscu
16	32	100.0	108	Q9UL70	Q9UL70 homo sapien
17	32	100.0	108	Q9UL77	Q9UL77 homo sapien
18	32	100.0	108	Q9UL83	Q9UL83 homo sapien
19	32	100.0	109	KV1T_HUMAN	P01612 homo sapien
20	32	100.0	109	KV3F_HUMAN	P01624 homo sapien
21	32	100.0	109	Q9UL85	Q9UL85 homo sapien
22	32	100.0	114	KV1A_MOUSE	P01632 mus muscu
23	32	100.0	114	KV4A_HUMAN	P01625 homo sapien
24	32	100.0	115	KV3I_HUMAN	P04433 homo sapien
25	32	100.0	116	KV3J_HUMAN	P04434 homo sapien
26	32	100.0	116	AAR11065	Aar11065 mus muscu
27	32	100.0	117	KV1I_HUMAN	P01601 homo sapien
28	32	100.0	117	KV1J_HUMAN	P01602 homo sapien
29	32	100.0	118	AAR11001	Aar11001 mus muscu
30	32	100.0	121	KV40_HUMAN	P06312 homo sapien
31	32	100.0	129	KV1W_HUMAN	P04431 homo sapien

32	32	100.0	129	1	KV1X_HUMAN	P04432 homo sapien
33	32	100.0	133	1	KV4B_HUMAN	P06313 homo sapien
34	32	100.0	134	1	KV4C_HUMAN	P06314 homo sapien
35	32	100.0	136	1	KV5B_MOUSE	P01634 mus muscu
36	32	100.0	174	2	BAC03964	Bac03964 homo sapi
37	32	100.0	234	2	AAH30813	AAH30813 homo sapi
38	32	100.0	236	2	Q6PIH7	Q6PIH7 homo sapien
39	32	100.0	236	2	Q6FIT5	Q6FIT5 homo sapien
40	32	100.0	236	2	Q6GMW1	Q6GMW1 homo sapien
41	32	100.0	236	2	Q6GMX0	Q6GMX0 homo sapien
42	32	100.0	236	2	Q6GMX8	Q6GMX8 homo sapien
43	32	100.0	236	2	Q6GMX9	Q6GMX9 homo sapien
44	32	100.0	236	2	Q7Z3Y4	Q7Z3Y4 homo sapien
45	32	100.0	236	2	AAH29444	AAH29444 homo sapi

ALIGNMENTS

RESULT 1

Q7VR58 PRELIMINARY; PRT; 78 AA.
AC Q7VR58;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Major outer membrane lipoprotein.
GN Name=lp; OrderedLocusNames=Bfl1364;
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22784745; PubMed=12886019;
RA Gil R., Silva F.J., Zientz E., Delmorte F., Gonzalez-Candelas F.,
RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
RA van Ham R.C.H.J., Gross R., Moya A.;
RT "The genome sequence of Blochmannia floridanus: comparative analysis
of reduced genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
DR EMBL; BX248595; CAD83431.1; -;
SK Complete proteome; Lipoprotein.
SQ SEQUENCE 78 AA; 8906 MW; 4AA330089F0A0EC2 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7

Db 9 FTLTSS 15

RESULT 2

AAR10995 PRELIMINARY; PRT; 81 AA.
ID AAR10995;
AC AAR10995;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE ANA immunoglobulin kappa light chain (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6.S1el; TISSUE=Spleen;
RA Liang Z., Xie C., Chen C., Kreska D., Hsu K., Zhou J.X., Mohan C.;
RT "Antinuclear autoantibodies from B6.S1el mice.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AY436835; AAR10995.1; -.

Qy 1 FTLTSS 7

DR PIR; PH0867; PH0867.
 DR PIR; S16840; S16840.
 DR PIR; S31977; S31977.
 DR PIR; S34083; S34083.
 DR PIR; S34086; S34086.
 DR HSSP; P01607; 1BWV.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 1
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11520 MW; 4B843E9C5B577F16 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
 |||||
 Db 71 FTLTSS 77

RESULT 7

ID Q9ERZ9 PRELIMINARY; PRT; 107 AA.
 AC Q9ERZ9;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Anti human TNF-alpha light chain variable region (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
 RT "Construction and sequencing of the single-chain antibody gene of a
 human TNF-alpha specific monoclonal antibody.";
 RL Di 4 Jun Yi ba Xue Xue Bao 19:373-376(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
 RT "Cloning and sequencing of the light chain fragment of variable region
 genes of an anti-hTNF-a monoclonal antibody.";
 RL Xibao Yu Fenzi Mianyixue Zazhi 12:21-26(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF262753; AAG33804.1;
 DR PDB; 2AP2; X-ray; A/C=1-107.
 DR PDB; 43C9; X-ray; A/C/E/G=1-107.
 DR PDB; 43CA; X-ray; A/C/E/G=1-107.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 FT NON_TER 107
 SQ SEQUENCE 107 AA; 11784 MW; 2B15BEA6604A26C3 CRC64;

Query Match 100.0%; Score 32; DB 2; Length 107;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
 |||||
 Db 74 FTLTSS 80

RESULT 8

KV1F_HUMAN
 ID KV1F_HUMAN STANDARD; PRT; 108 AA.
 AC P01598;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region EU.
 DE Ig kappa chain V-I region EU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71064023; PubMed=5489770;
 RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
 acid sequence of the light chain.";
 RL Biochemistry 9:3155-3161(1970).
 RN [2]
 RP DISULFIDE BOND.
 RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 Intrachain disulfide bonds";
 RL Biochemistry 9:3188-3196(1970).
 CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
 DR PIR; A30562; K1HWU.
 DR HSSP; P01607; 1BWV.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
 |||||
 Db 71 FTLTSS 77

RESULT 9

KV1G_HUMAN
 ID KV1G_HUMAN STANDARD; PRT; 108 AA.
 AC P01599;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region Gal.
 DE Ig kappa chain V-I region Gal.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal IgM-immunoglobulin
FT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504 (1973).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
DR PIR; A01867; KIHUHL.
DR HSSP; P01607; 1BWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; C1AD3CB0F600FF73 CRC64;
Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
Db 71 FTLTSS 77
RESULT 10
KVIL HUMAN
ID KVIL HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01868; KIHUHL.
DR PDB; 1F6L; X-ray; L=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;

Immunoglobulin V region.
KW DOMAIN 1 23
KW DOMAIN 24 34
KW DOMAIN 35 49
KW DOMAIN 50 56
KW DOMAIN 57 88
KW DOMAIN 89 97
KW DOMAIN 98 107
KW DISULFID 23 88
KW NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
Db 71 FTLTSS 77
RESULT 11
KVIL HUMAN
ID KVIL HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Wes.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81092279; PubMed=6778806;
RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
RT "Preparative separation of the tryptic hydrolysate of a protein by
RT high-pressure liquid chromatography. The primary structure of a
RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein Wes).";
RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598 (1980).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01877; KIHUWS.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60B45 CRC64;
Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLTSS 7
Db 71 FTLTSS 77


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RESULT 12
KV5Q MOUSE
ID KV5Q MOUSE STANDARD; PRT; 108 AA.
AC P01650;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region UPC 61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; A92808; KVM561.
DR HSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11809 MW; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

RESULT 13
KV5R MOUSE
ID KV5R MOUSE STANDARD; PRT; 108 AA.
AC P01651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region EPC 109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79195288; PubMed=109517;
RA Vrana M., Rudikoff S., Potter M.;
RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL J. Immunol. 122:1905-1910(1979).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; B92808; KVM509.
DR HSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.

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DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11876 MW; 35C116BD60F79310 CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

RESULT 14
KV5S MOUSE
ID KV5S MOUSE STANDARD; PRT; 108 AA.
AC P01652;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region J606.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Slankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; A92811; KVM506.
DR HSP; P01607; 1BMW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11810 MW; 8DE4DD31076F2AFB CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
DB 71 FTLTSS 77

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RESULT 15
KVST MOUSE
ID KVST MOUSE STANDARD; PRT; 108 AA.
AC P01653;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-V region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP MEDLINE=82093361; PubMed=6798111;
RA Johnson N., Sankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
RT binding proteins.";
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC bind beta(2-1)-fructofuranosyl moieties (inulin).
DR PIR; B92811; KVM382.
DR HSP; P01607; 1BWV.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DOMAIN 98 108 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 32; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTSS 7
Db 71 FTLTSS 77

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Search completed: November 4, 2004, 00:53:55
Job time : 104 secs

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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:33:03 ; Search time 60 Seconds

(without alignments)
41.852 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 23Sep04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	32	100.0	13	5 ADG67499	ADG67499 Humanised
2	32	100.0	13	5 ADG67501	ADG67501 Humanised
3	32	100.0	13	5 ADG67500	ADG67500 Humanised
4	32	100.0	13	5 ADG67502	ADG67502 Humanised
5	32	100.0	19	6 AAE38112	AAE38112 Human COU
6	32	100.0	32	2 AAE87043	AAE87043 Human gro
7	32	100.0	32	2 AAY52745	AAY52745 Humanised
8	32	100.0	32	4 AAB98286	AAB98286 Anti-A33
9	32	100.0	32	4 AAB98288	AAB98288 Anti-A33
10	32	100.0	32	4 AAB97666	AAB97666 A33 anti
11	32	100.0	32	4 AAB97668	AAB97668 A33 anti
12	32	100.0	32	5 AAB98287	AAB98287 Human ant
13	32	100.0	32	5 AAE19672	AAE19672 Human gro
14	32	100.0	32	5 AAB62658	AAB62658 Human imm
15	32	100.0	32	5 AAB62688	AAB62688 Human imm
16	32	100.0	32	5 AAB62673	AAB62673 Human imm
17	32	100.0	32	5 AAU70396	AAU70396 Human lig
18	32	100.0	32	5 AAU70408	AAU70408 Human lig
19	32	100.0	32	5 AAU70436	AAU70436 Mouse lig
20	32	100.0	32	5 AAU17650	AAU17650 Human PAP
21	32	100.0	32	6 ABO10698	ABO10698 Deimmunis
22	32	100.0	32	6 ABR44642	ABR44642 Murine J5
23	32	100.0	32	6 AAE38099	AAE38099 Human COU
24	32	100.0	32	7 ABO33922	ABO33922 Anti-GPI-
25	32	100.0	32	7 ABO33921	ABO33921 Anti-GPI-

26	32	100.0	32	7 ABO33924	ABO33924 Anti-GPI-
27	32	100.0	32	8 ADH17942	ADH17942 Human 15H
28	32	100.0	32	8 ADH17975	ADH17975 Human mod
29	32	100.0	32	8 ADH17983	ADH17983 Human mod
30	32	100.0	36	7 ABW01925	ABW01925 Human rhu
31	32	100.0	42	5 ABG98296	ABG98296 Antibody
32	32	100.0	42	5 ABG98294	ABG98294 Human ant
33	32	100.0	42	5 ABG98288	ABG98288 Human ant
34	32	100.0	42	5 ABG98290	ABG98290 Antibody
35	32	100.0	50	5 ABG30482	ABG30482 Human ant
36	32	100.0	70	7 ABG75305	ABG75305 Human sub
37	32	100.0	70	8 ABM79517	ABM79517 Human DPK
38	32	100.0	74	2 AAR62921	AAR62921 Human cyt
39	32	100.0	74	2 AAW62805	AAW62805 Amino aci
40	32	100.0	75	2 AAR62923	AAR62923 Human cyt
41	32	100.0	76	2 AAW80981	AAW80981 Variable
42	32	100.0	76	6 ABO04843	ABO04843 Human epi
43	32	100.0	79	8 ADL35149	ADL35149 CEA4-8A a
44	32	100.0	79	8 ADL35148	ADL35148 Humanised
45	32	100.0	80	6 ABO10701	ABO10701 Deimmunis

ALIGNMENTS

RESULT 1

ADG67499

ID ADG67499 standard; peptide; 13 AA.

XX AC ADG67499;

XX AC

DT 11-MAR-2004 (first entry)

XX

DE Humanised anti-Tac antibody MHC class II binding peptide #61.

XX

KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;

KM immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX

PN WO200269232-A2.

XX

PD 06-SEP-2002.

XX

PF 18-FEB-2002; 2002WO-EP001688.

XX

PR 19-FEB-2001; 2001EP-00103954.

PR

PR 08-MAR-2001; 2001EP-00105777.

PR

PR 15-MAR-2001; 2001EP-00106536.

PR

PR 15-MAR-2001; 2001EP-00106538.

PR

PR 20-MAR-2001; 2001EP-00106899.

PR

PR 20-MAR-2001; 2001EP-00107012.

PR

PR 27-MAR-2001; 2001EP-00107568.

PR

PR 25-APR-2001; 2001EP-00110220.

PR

PR 30-MAY-2001; 2001EP-00113228.

PR

PR 19-OCT-2001; 2001EP-00124965.

PR

PR 12-NOV-2001; 2001EP-00126859.

XX

XX (MERE) MERCK PATENT GMBH.

PA

XX Carr FU, Carter G, Jones T, Williams S, Hamilton A;

XX

PI WPI; 2002-750424/81.

XX

XX Identifying potential T-cell epitope peptides within the amino acid

PT sequence of a biological molecule, useful for preparing a biological

PT molecule with reduced immunogenicity, comprises determining peptide

PT binding to MHC molecules.

XX

XX Example 20; Page 60; 85pp; English.

PS The invention relates to a novel method for identifying one or more

XX potential T-cell epitope peptides within the amino acid sequence of a

CC

CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;
 SQ Query Match 100.0%; Score 32; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7
 Db 7 FTLTISS 13
 |||||

RESULT 2
 ADG67501
 ID ADG67501 standard; peptide; 13 AA.

XX AC ADG67501;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #63.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 XX immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001688.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00106899.

XX PR 20-MAR-2001; 2001EP-00107012.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 30-MAY-2001; 2001EP-00110220.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

XX PF 2002-750424/81.

XX PT Identifying potential T-cell epitope peptides within the amino acid

XX PT sequence of a biological molecule, useful for preparing a biological

XX PT molecule with reduced immunogenicity, comprises determining peptide

XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX PS The invention relates to a novel method for identifying one or more

CC potential T-cell epitope peptides within the amino acid sequence of a
 CC biological molecule by determining the binding of the peptides to major
 CC histocompatibility complex (MHC) molecules using in vitro or in silico
 CC techniques or biological assays. The method of the invention is useful
 CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;
 SQ Query Match 100.0%; Score 32; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7
 Db 7 FTLTISS 13
 |||||

RESULT 2
 ADG67501
 ID ADG67501 standard; peptide; 13 AA.

XX AC ADG67501;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #63.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 XX immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001688.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00106899.

XX PR 20-MAR-2001; 2001EP-00107012.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 30-MAY-2001; 2001EP-00110220.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

XX PF 2002-750424/81.

XX PT Identifying potential T-cell epitope peptides within the amino acid

XX PT sequence of a biological molecule, useful for preparing a biological

XX PT molecule with reduced immunogenicity, comprises determining peptide

XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX PS The invention relates to a novel method for identifying one or more

CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
 CC their fragments with reduced immunogenicity. The potential T-cell epitope
 CC peptide within the amino acid sequence of a parent immunogenically non-
 CC modified biological molecule identified is useful for preparing a
 CC biological molecule with reduced immunogenicity and having a retained
 CC desired biological activity, where the T-cell epitope is a 13mer peptide.
 CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;

SQ Query Match 100.0%; Score 32; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLTISS 7

Db 3 FTLTISS 9

RESULT 3

ADG67500

ID ADG67500 standard; peptide; 13 AA.

XX AC ADG67500;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #62.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
 XX immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001688.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00106899.

XX PR 20-MAR-2001; 2001EP-00107012.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 30-MAY-2001; 2001EP-00110220.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;

XX PF 2002-750424/81.

XX PT Identifying potential T-cell epitope peptides within the amino acid

XX PT sequence of a biological molecule, useful for preparing a biological

XX PT molecule with reduced immunogenicity, comprises determining peptide

XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX PS The invention relates to a novel method for identifying one or more

XX CC potential T-cell epitope peptides within the amino acid sequence of a

XX CC biological molecule by determining the binding of the peptides to major

CC modified biological molecule identified is useful for preparing a
CC biological molecule with reduced immunogenicity and having a retained
CC desired biological activity, where the T-cell epitope is a 13mer peptide.
CC The present sequence is used in the exemplification of the invention.

XX SQ Sequence 13 AA;
Query Match 100.0%; Score 32; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;
Qy 1 FTLTIS 7
Db 4 FTLTIS 10

RESULT 4
ADG67502
ID ADG67502 standard; peptide; 13 AA.

XX AC

ADG67502;

XX DT 11-MAR-2004 (first entry)

XX DE Humanised anti-Tac antibody MHC class II binding peptide #64.

XX KW human; mouse; T-cell epitope; major histocompatibility complex; MHC;
XX KW immunogenicity; MHC class II; antibody.

XX OS Homo sapiens.

XX PN WO200269232-A2.

XX PD 06-SEP-2002.

XX PF 18-FEB-2002; 2002WO-EP001698.

XX PR 19-FEB-2001; 2001EP-00103954.

XX PR 08-MAR-2001; 2001EP-00105777.

XX PR 15-MAR-2001; 2001EP-00106536.

XX PR 15-MAR-2001; 2001EP-00106538.

XX PR 20-MAR-2001; 2001EP-00106899.

XX PR 20-MAR-2001; 2001EP-00107012.

XX PR 27-MAR-2001; 2001EP-00107568.

XX PR 25-APR-2001; 2001EP-00110220.

XX PR 30-MAY-2001; 2001EP-00113228.

XX PR 19-OCT-2001; 2001EP-00124965.

XX PR 12-NOV-2001; 2001EP-00126859.

XX PA (MERE) MERCK PATENT GMBH.

XX PI Carr EJ, Carter G, Jones T, Williams S, Hamilton A;

XX DR WPI; 2002-750424/81.

XX DR Identifying potential T-cell epitope peptides within the amino acid
XX PT sequence of a biological molecule, useful for preparing a biological
XX PT molecule with reduced immunogenicity, comprises determining peptide
XX PT binding to MHC molecules.

XX PS Example 20; Page 60; 85pp; English.

XX CC The invention relates to a novel method for identifying one or more
XX CC potential T-cell epitope peptides within the amino acid sequence of a
XX CC biological molecule by determining the binding of the peptides to major
XX CC histocompatibility complex (MHC) molecules using in vitro or in silico
XX CC techniques or biological assays. The method of the invention is useful
XX CC for preparing a polypeptide, a protein, a fusion protein, an antibody or
XX CC their fragments with reduced immunogenicity. The potential T-cell epitope
XX CC peptide within the amino acid sequence of a parent immunogenically non-
XX CC modified biological molecule identified is useful for preparing a
XX CC biological molecule with reduced immunogenicity and having a retained
XX CC desired biological activity, where the T-cell epitope is a 13mer peptide.

CC The present sequence is used in the exemplification of the invention.
XX SQ Sequence 13 AA;

Query Match 100.0%; Score 32; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTIS 7
Db 1 FTLTIS 7

RESULT 5
AAR38112
ID AAR38112 standard; peptide; 19 AA.

XX AC

AAR38112;

XX DT 06-NOV-2003 (first entry)

XX DE Human COU-1 antibody VL FR3 peptide #4.

XX KW Human; cancer-associated epitope; cytokeratin K8; cytokeratin K18; VL;
XX KW adenocarcinoma; therapy; cancer; antibody; light chain variable region;
XX KW framework region; FR.

XX OS Homo sapiens.

XX PN WO2003057168-A2.

XX PD 17-JUL-2003.

XX PF 03-JAN-2003; 2003WO-US000297.

XX PR 03-JAN-2002; 2002US-0345208P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Ditzel H, Jensenius JC;

XX DR WPI; 2003-598315/56.

XX PT Novel isolated cancer-associated epitope comprising two separate
XX PT polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
XX PT polypeptide, useful as component of vaccine for preventing or treating
XX PT adenocarcinoma.

XX PS Claim 15; Page 37; 155pp; English.

XX CC The invention provides a cancer-associated epitope comprising two
XX CC separate polypeptides, a cytokeratin 8 polypeptide and a cytokeratin 18
XX CC polypeptide. Vaccine composition of the invention is useful for treating
XX CC or preventing colon adenocarcinoma, ovarian adenocarcinoma, renal
XX CC adenocarcinoma, mammary adenocarcinoma, lung adenocarcinoma, pancreatic
XX CC adenocarcinoma or non-seminoma testis carcinoma. The invention is also
XX CC useful for preparing a medicament for treating or preventing cancer in a
XX CC mammal. The present sequence is human COU-1 cancer-associated epitope
XX CC antibody VL (light chain variable region) FR (framework region) peptide
XX SQ Sequence 19 AA;

Query Match 100.0%; Score 32; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTIS 7
Db 2 FTLTIS 8

RESULT 6
AAR87043

ID AAR87043 standard; peptide; 32 AA.
 AC AAR87043;
 XX
 DT 25-JUN-1996 (first entry)
 XX
 DE Human group I light chain framework 3.
 XX
 DE Humanised antibody; interleukin-5; IL-5; recombinant antibody;
 KW antibody engineering; monoclonal antibody; NAb; 39D10; CDR;
 KW complementarity determining region; light chain; framework; eosinophilia;
 KW allergy; asthma.
 XX
 KW Homo sapiens.
 OS
 XX WO9535375-A1.
 PN
 XX 28-DEC-1995.
 PD
 XX 16-JUN-1995; 95WO-GB001411.
 PF
 XX 17-JUN-1994; 94GB-00012230.
 PR
 XX (CLLT) CELLTech THERAPEUTICS LTD.
 PA
 XX Entage JS, Bodmer WM, Athwal DS;
 PI
 XX WPI; 1996-058412/06.
 DR
 XX Anti-human IL-5 recombinant antibody - useful for preventing or reducing
 PT eosinophilia and for treating certain allergic diseases, esp. asthma.
 PT
 PS Example 3; Fig 3; 69pp; English.
 XX
 CC Framework regions (AAR87041-44) of human group I (gp1) germ line antibody
 CC light chain showed homology to corresponding regions (AAR87045-48,
 CC respectively) of the rat anti-human interleukin-5 monoclonal antibody
 CC 39D10 light chain (see AAR87040). This homology was utilised in the
 CC prodn. of a humanised 39D10 VL (AAR87057) in which rat 39D10 VL
 CC complementarity determining regions were grafted into the human gp1
 CC framework
 CC
 XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 DB 15 FTLTISS 21
 DE
 RESULT 7
 AAY52745
 ID AAY52745 standard; peptide; 32 AA.
 XX
 AC AAY52745;
 XX
 DT 26-JAN-2000 (first entry)
 XX
 DE Humanised ATR-5 L chain V region FR3 for a.
 XX
 KW Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
 KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
 KW disseminated intravascular coagulation; immunogenicity; chimeric.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX WO9951743-A1.
 PN
 XX 14-OCT-1999.
 PD

XX 02-APR-1999; 99WO-JP001768.
 PF
 XX 03-APR-1998; 98JP-00091850.
 PR
 XX (CHUS) CHUGAI SEIYAKU KK.
 PA
 XX Sato K, Adachi H, Yabuta N;
 PI
 XX WPI; 1999-620204/53.
 DR
 XX Humanised antibody recognizing human tissue factor, used for treatment of
 PT disseminated intravascular coagulation.
 PT
 PS Claim 17; Page 270; 291pp; Japanese.
 PS
 XX The present invention describes chimeric antibody (Ab) heavy (H) chains
 CC containing the variable region of the H chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrf) and the constant region of the H
 CC chain of a human Ab. The variable region is one of six specified
 CC sequences (which are the H chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
 CC containing the variable region of the L chain of a mouse monoclonal Ab
 CC recognising human tissue factor (hrf) and the constant region of the L
 CC chain of a human Ab, the variable region being one of six specified
 CC sequences (which are the L chain variable regions from mouse monoclonal
 CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
 CC and prevention of thrombotic disease, especially of disseminated
 CC intravascular coagulation (DIC). The humanised antibody has the high hrf
 CC binding activity of the mouse monoclonal antibody but greatly reduced
 CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX SQ Sequence 32 AA;
 Query Match 100.0%; Score 32; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 DB 15 FTLTISS 21
 DE
 RESULT 8
 AAB98286
 ID AAB98286 standard; peptide; 32 AA.
 XX
 AC AAB98286;
 XX
 DT 20-AUG-2001 (first entry)
 DT
 XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.
 DE
 XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytostatic; anticancer; colon cancer; stomach cancer.
 XX
 OS Homo sapiens.
 OS
 XX WO200130393-A2.
 PN
 XX 03-MAY-2001.
 PD
 XX 20-OCT-2000; 2000WO-US029289.
 PF
 XX 22-OCT-1999; 99US-00425638.
 PR
 PR 04-APR-2000; 2000US-00543004.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SCRI) SCRIPPS RES INST.
 XX

PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 DR WPI; 2001-328613/34.
 XX
 XX Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 PT immunoglobulin product.
 XX
 XX Claim 16; Page 40; 85pp; English.
 PS
 XX The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an anticancer
 CC agent (I) conjugated to an immunoglobulin product (II) that binds
 CC specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98262 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the present
 CC invention
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 32; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 DB 15 FTLTISS 21
 DE 20-AUG-2001 (first entry)
 DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.
 XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytostatic; anticancer; colon cancer; stomach cancer.
 XX
 OS Homo sapiens.
 XX
 FN WO200130393-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029289.
 XX
 PR 22-OCT-1999; 99US-00425638.
 PR 04-APR-2000; 2000US-00543004.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
 DR WPI; 2001-328613/34.
 XX
 XX Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 PT immunoglobulin product.
 XX
 XX Claim 16; Page 40; 85pp; English.

CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an anticancer
 CC agent (I) conjugated to an immunoglobulin product (II) that binds
 CC specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98262 to
 CC AAB98274. (I) has cytostatic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the present
 CC invention
 XX
 XX Sequence 32 AA;
 SQ
 Query Match 100.0%; Score 32; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FTLTISS 7
 DB 15 FTLTISS 21
 DE 08-AUG-2001 (first entry)
 DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:92.
 XX Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW immunoreact; anti A33 antigen antibody; immunoglobulin.
 XX
 OS Homo sapiens.
 XX
 FN WO200131065-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US029026.
 XX
 PR 22-OCT-1999; 99US-00425638.
 PR 04-APR-2000; 2000US-00543004.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Barbas CF, Rader C;
 DR WPI; 2001-328657/34.
 XX
 XX Preparing humanized rabbit antibodies that specifically immunoreact with
 PT a particular antigen using display technology for expressing libraries of
 PT antibody domains and fine tuning variable domain regions.
 XX
 XX Example 9; Page 39; 62pp; English.
 PS
 XX The present invention describes a method for preparing a humanised rabbit
 CC antibody that specifically immunoreacts with a particular antigen. The
 CC method comprises expressing a library of antibodies comprising one or
 CC more complementarity determining region (CDR) from the variable domain
 CC sequences that specifically immunoreact with the antigen grafted into
 CC framework regions from humans, and selecting the antibodies that react
 CC with the antigen. The method is useful for humanising non-human mammalian
 CC antibodies, which can be used for the treatment of a variety of diseases.
 CC The present sequence represents an A33 antigen binding immunoglobulin
 CC product VLFR3 peptide which is given in an example from the present
 CC invention
 XX
 XX Sequence 32 AA;

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLTSS 7
| | | | |
Db 15 FTLTSS 21

RESULT 11

AB97668
ID AAB97668 standard; peptide; 32 AA.

AC AAB97668;

XX 08-AUG-2001 (first entry)

DE A33 antigen binding immunoglobulin product VLF33 peptide SEQ ID NO:94.

KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody; immunoglobulin.

XX Homo sapiens.

XX WO200131065-A1.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US029026.

XX 22-OCT-1999; 99US-00425638.

XX 04-APR-2000; 2000US-00543004.

XX (SCRI) SCRIPPS RES INST.

XX Barbas CF, Rader C;

XX WPI; 2001-328657/34.

XX Preparing humanized rabbit antibodies that specifically immunoreact with
PT a particular antigen using display technology for expressing libraries of
PT antibody domains and fine tuning variable domain regions.

XX Example 9; Page 39; 62pp; English.

XX The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human mammalian
CC antibodies, which can be used for the treatment of a variety of diseases.
CC The present sequence represents an A33 antigen binding immunoglobulin
CC product VLF33 peptide which is given in an example from the present
CC invention

XX Sequence 32 AA;

Query Match 100.0%; Score 32; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 FTLTSS 7
| | | | |
Db 15 FTLTSS 21

RESULT 12

AB98287
ID ABG98287 standard; peptide; 32 AA.

XX

AC ABG98287;

XX 08-JAN-2003 (first entry)

DE Human antibody 012/V3b germline kappa chain variable region FR3/FR4 #1.

XX Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40;
KW T-cell activation; B-cell differentiation; framework region;
KW cellular immune response; gene therapy; graft rejection; human; FR;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
KW asthma; multiple sclerosis; allergy; diabetes mellitus;
KW systemic lupus erythematosus; graft-versus-host disease.

XX Homo sapiens.

XX WO200194586-A2.

XX 13-DEC-2001.

XX 06-JUN-2001; 2001WO-US018098.

XX 06-JUN-2000; 2000US-0209584P.

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Pan LZ, Hanna N, Rastetter WH, Kloetzer WS;

XX WPI; 2002-188261/24.

XX New antibodies binding to an epitope on gp39, useful for preventing graft
PT rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or
PT multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
PT disease).

XX Disclosure; Page 46; 130pp; English.

XX The invention relates to an antibody which binds to an epitope on gp39,
CC is new, where the epitope is distinct from the epitope bound by IDEC-131,
CC and the antibody has a non-agonistic effect on T-cell activation and
CC inhibits gp39/CD40 interaction. Also included are: (1) an improved method
CC of creating a disease by modulating gp39 expression or inhibiting the
CC gp39/CD40 interaction comprising administering an antibody specific for
CC gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-
CC cell activation; (2) an antibody which antagonises B-cell differentiation
CC and antibody production, and is non-agonistic of T-cell activation; (3)
CC a DNA sequence which encodes an antibody defined above; (4) an expression
CC vector, which contains a DNA sequence of (3); (5) a method of suppressing
CC humoral and/or cellular immune responses against cells or vectors
CC administered during cell or gene therapy comprising further administering
CC prior, during or after gene therapy, an antibody defined above; and (6)
CC an improved method of treatment which involves the transplantation of
CC cells, tissues or organs of the same or different species into a subject,
CC where the improvement comprises administering an antibody defined above
CC prior, during or after transplantation, to suppress immune responses
CC against the transplanted cell, tissue or organ, or to suppress immune
CC responses elicited by the transplanted cell, tissue or organ against the
CC host. The antibody is useful for preventing graft rejection, and for
CC treating autoimmune diseases, e.g., rheumatoid arthritis, multiple
CC sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions,
CC diabetes mellitus, or systemic lupus erythematosus, as well as non-
CC autoimmune diseases such as graft-versus-host disease (many other
CC diseases and conditions are given in the specification). The antibodies
CC are also useful in gene or cellular therapy, and to inhibit humoral and
CC cellular immune responses against viral vectors. The present sequence is
CC a framework region (FR) fragment of a human anti-gp39 antibody used to
CC determine which amino acids should be humanised in a mouse anti-gp39
CC molecule

XX Sequence 32 AA;

Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;


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OY      1 FTLTISS 7
Db      15 FTLTISS 21
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RESULT 13
AAE19672
ID AAE19672 standard; peptide; 32 AA.
XX
AC AAE19672;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human group 1 consensus peptide #3.
XX
KW Human; tumour necrosis factor 40; TNF40; osteopathic; cardiac; CDR;
KW complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
KW congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
KW Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
KW cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
KW inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
KW neoplasia therapy; immunomodulator; vulnery; graft rejection.
XX
OS Homo sapiens.
XX
PN WO200194585-A1.
XX
PD 13-DEC-2001.
XX
PF 05-JUN-2001; 2001WO-GB002477.
XX
PR 06-JUN-2000; 2000GB-00013810.
XX
PA (CELL-) CELLTech R & D LTD.
XX
PI Athwal DS, Brown DT, Weir ANC, Popplewell AG, Chapman AP;
PI King DU;
XX
DR WPI; 2002-216732/27.
XX
PT New antibody specific for human tumor necrosis factor (TNF)-alpha, useful
PT for treating TNF-alpha-mediated diseases, e.g. congestive heart failure,
PT septic or endotoxemic shock, cachexia, adult respiratory distress syndrome.
XX
PS Example 1; Fig 1; 119pp; English.
XX
CC The invention relates to an antibody molecule having specificity for
CC human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light
CC chain. The antibody or the compound comprising the antibody is useful for
CC treating or manufacturing a medicament for treating a pathology mediated
CC by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated
CC diseases which can be treated by the antibody include sepsis, congestive
CC heart failure, septic or endotoxemic shock, cachexia, adult respiratory
CC distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies,
CC psoriasis, tuberculosis, inflammatory bone disorders, blood coagulation
CC disorders, burns, rejection episodes following organ or tissue
CC transplant, Crohn's disease and autoimmune diseases, such as thyroiditis.
CC The antibodies may also be used to reduce the side effects associated
CC with TNFalpha generation during neoplasia therapy, to eliminate or reduce
CC shock-related symptoms associated with the treatment or prevention of
CC graft rejection by use of an anti-lymphocyte antibody for treating multi
CC organ failure, or in the diagnosis and imaging of disease states
CC involving elevated levels of TNF alpha. The present sequence is human
CC group 1 consensus peptide used in the exemplification of the invention
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 FTLTISS 7
Db      15 FTLTISS 21
        |||||
RESULT 14
ABP62658
ID ABP62658 standard; peptide; 32 AA.
XX
AC ABP62658;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein framework sequence #166.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-US002303.
XX
PR 26-JAN-2001; 2001US-0264451P.
XX
PA (SCRI ) SCRIPPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
DR WPI; 2002-599801/64.
XX
PT New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
PS Claim 4; Fig 17; 308pp; English.
XX
CC The present invention relates to human immunopolypeptides, produced by a
CC phage transacted cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought
CC to be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 32 AA;
Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 FTLTISS 7
Db      15 FTLTISS 21
        |||||
RESULT 15
ABP62688
ID ABP62688 standard; peptide; 32 AA.
XX
AC ABP62688;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein framework sequence #196.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;

```

KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
XX Homo sapiens.
XX WO200259340-A1.
XX
XX 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-US002303.
XX
XX 26-JAN-2001; 2001US-0264451P.
XX
XX (SRI) SCRIPPS RES INST.
XX
XX Maruyama T, Jones IM, Burton DR, Fox RI;
XX
XX WPI; 2002-599801/64.
XX
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
XX Claim 4; Fig 17; 308pp; English.
XX
XX The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
XX Sequence 32 AA;

Query Match 100.0%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTITISS 7
Db 15 FTITISS 21

Search completed: November 4, 2004, 00:47:39
Job time : 62.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 4, 2004, 00:48:50 ; Search time 72.3333 Seconds
(without alignments)
31.376 Million cell updates/sec

Title: US-09-712-819D-1

Perfect score: 32

Sequence: 1 FTLTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	100.0	13	16	US-10-468-496-1991
2	32	100.0	13	16	US-10-468-496-1992
3	32	100.0	13	16	US-10-468-496-1993
4	32	100.0	13	16	US-10-468-496-1994
5	32	100.0	32	9	US-09-855-271-13
6	32	100.0	32	9	US-09-828-708-95
7	32	100.0	32	9	US-09-828-708-96
8	32	100.0	32	9	US-09-828-708-98
9	32	100.0	32	9	US-09-943-559-91
10	32	100.0	32	10	US-09-874-141-15
11	32	100.0	32	10	US-09-875-221A-91
12	32	100.0	32	10	US-09-563-222-76
13	32	100.0	32	10	US-09-563-222-88

Sequence 116, App
Sequence 35, Appl
Sequence 15, Appl
Sequence 87, Appl
Sequence 51, Appl
Sequence 84, Appl
Sequence 92, Appl
Sequence 129, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 248, App
Sequence 251, App
Sequence 254, App
Sequence 257, App
Sequence 260, App
Sequence 263, App
Sequence 266, App
Sequence 269, App
Sequence 272, App
Sequence 275, App
Sequence 76, Appl
Sequence 86, Appl
Sequence 110, App
Sequence 5, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 17, Appl
Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-10-468-496-1991
; Sequence 1991, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1991
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1991

Query Match 100.0%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 7 FTLTISS 13

RESULT 2

US-10-468-496-1992
; Sequence 1992, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1992
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1992

Query Match 100.0%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 3 FTLTISS 9

RESULT 4

US-10-468-496-1994
; Sequence 1994, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1994
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope

US-10-468-496-1994

Query Match 100.0%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLTISS 7
|||||
Db 4 FTLTISS 10

RESULT 3

US-10-468-496-1993
; Sequence 1993, Application US/10468496
; Publication No. US20040180386A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496

Query Match 100.0%; Score 32; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 1 FTLTSS 7

RESULT 5

US-09-855-271-13
; Sequence 13, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark W
; APPLICANT: Ahwal, Diljeet Singh
; APPLICANT: Emage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0088
; CURRENT APPLICATION NUMBER: US/09/855,271
; CURRENT FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/347,061
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-09-855-271-13

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
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Db 15 FTLTSS 21

RESULT 6

US-09-828-708-95
; Sequence 95, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-95

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 15 FTLTSS 21

RESULT 7

US-09-828-708-96
; Sequence 96, Application US/09828708
; Patent No. US20020146753A1

; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-96

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
|||||
Db 15 FTLTSS 21

RESULT 8

US-09-828-708-98
; Sequence 98, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-98

Query Match 100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTSS 7
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Db 15 FTLTSS 21

RESULT 9

US-09-949-559-91
; Sequence 91, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Ahwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06

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; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework L3
US-09-949-559-91

Query Match          100.0%; Score 32; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 10
US-09-874-141-15
; Sequence 15, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL
; APPLICANT: PAN, LI-ZHEN
; APPLICANT: HANNA, NABIL
; APPLICANT: RASTETTER, WILLIAM H.
; APPLICANT: KLOETZER, WILLIAM S.
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0280632
; CURRENT APPLICATION NUMBER: US/09/874,141
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,584
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-141-15

Query Match          100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 11
US-09-875-221A-91
; Sequence 91, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weit, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Card-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human group 1 consensus framework L3
US-09-875-221A-91

Query Match          100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 12
US-09-563-222-76
; Sequence 76, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-76

Query Match          100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21

RESULT 13
US-09-563-222-88
; Sequence 88, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-563-222-88

Query Match          100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLTISS 7
Db 15 FTLTISS 21
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Db          15 FTLTISS 21

RESULT 14
US-09-563-222-116
; Sequence 116, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-116

Query Match      100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      15 FTLTISS 21

RESULT 15
US-09-791-551-35
; Sequence 35, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 35
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-35

Query Match      100.0%; Score 32; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 FTLTISS 7
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Db      15 FTLTISS 21

Search completed: November 4, 2004, 01:13:28
Job time : 73.3333 secs
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